

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 6, 2005, 10:32:12 ; Search time 180.906 Seconds
(without alignments)
686.395 Million cell updates/sec

Title: US-10-611-655-10
Perfect score: 944
Sequence: 1 MHGEGTFTSDVSSYLEGQAA.....VKCEGISLLAQTSHHHHH 176

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	630	66.7	161	1 THY1 HUMAN	P04216 homo sapien
2	624	66.1	161	2 Q5R508 PONY	Q5R508 pongo pygma
3	619	65.6	161	1 THY1 MACMU	Q62643 macaca mula
4	546	57.8	145	2 Q59GA0 HUMAN	Q59GA0 homo sapien
5	503	53.3	161	2 Q9WUR5 CAVPO	Q9WUR5 cavia porce
6	421	44.6	161	1 THY1 RAT	P01830 rattus norv
7	406.5	43.1	162	1 THY1 MOUSE	P01831 mus musculu
8	406.5	43.1	162	2 Q53XK2 MOUSE	Q53XK2 mus musculu
9	320	33.9	160	2 Q7T252 CHICK	Q7T252 gallus gall
10	305.5	32.4	160	1 THY1 CHICK	Q07212 gallus gall
11	244	25.8	60	2 Q9XT67 CANFA	Q9xt67 canis fami
12	157	16.6	45	2 Q6PPF4 CAPHI	Q6ppf4 capra hircu
13	157	16.6	176	1 GLUC SHREP	Q8mj25 o glucagon
14	157	16.6	180	1 GLUC BOVIN	P01272 b glucagon
15	157	16.6	180	1 GLUC CANFA	P29794 c glucagon
16	157	16.6	180	1 GLUC CAVPO	P05110 c glucagon
17	157	16.6	180	1 GLUC HUMAN	P01275 h glucagon
18	157	16.6	180	1 GLUC MSAU	P01273 m glucagon
19	157	16.6	180	1 GLUC MOUSE	P55095 m glucagon
20	157	16.6	180	1 GLUC OCTDE	P22890 s glucagon
21	157	16.6	180	1 GLUC PIG	P01274 s glucagon
22	157	16.6	180	1 GLUC RAT	P06883 r glucagon
23	157	16.6	180	2 Q53TP6 HUMAN	Q53TP6 homo sapien
24	145.5	15.4	124	2 Q6RYB1 9SAUR	Q6ryb1 agkistrodon
25	145	15.4	206	1 GLUC CHICK	P68259 g glucagon
26	144	15.3	80	2 Q61UF8 PHOSU	Q61uf8 phodopus su
27	139	14.7	145	2 Q6RYB5 NEOPS	Q6ryb5 neoceratodu
28	139	14.7	204	1 GLUC HELSU	Q12956 h glucagon
29	136	14.4	153	2 Q6RYB6 PRODO	Q6ryb6 proctoterus
30	135	14.3	255	2 Q6KB05 MOUSE	Q6kb05 mus musculu
31	125	13.2	103	1 GLUC RANCA	P15438 rana catesb

32	125	13.2	220	2 Q8UWL9 9NEOB	Q8uwl9 hoplobatr
33	123	13.0	120	2 Q6RYB7 ICTPU	Q6ryb7 ictalurus p
34	122	12.9	30	1 GLUCL ANGAN	P63294 anguilla an
35	122	12.9	30	1 GLUCL ANGRO	P63295 anguilla ro
36	122	12.9	122	1 GLUC2 LOPAM	P04092 lophius ame
37	122	12.9	123	2 Q6RYA9 9PERC	Q6rya9 sebastes ca
38	122	12.9	860	2 Q4RQY4 TETNG	Q4rqj4 tetraodon n
39	121	12.8	149	2 Q6RYB2 BUFMA	Q6ryb2 bufo marinu
40	121	12.8	266	1 GLUC1 XENLA	Q42143 xenopus lae
41	121	12.8	266	2 Q6DI24 XENTR	Q6di24 xenopus tro
42	118	12.5	487	2 Q65ZL2 9MURI	Q65z12 mus sp. fv/
43	116	12.3	219	1 GLUC2 XENLA	Q42144 xenopus lae
44	116	12.3	219	2 Q5D082 XENLA	Q5d082 xenopus lae
45	115	12.2	33	1 GLUC2_ORENI	P81027 oreochromis

ALIGNMENTS

RESULT 1
ID THY1 HUMAN STANDARD; PRT; 161 AA.
AC P04216; Q16008; Q9NSP1;
DT 20-MAR-1987 (Rel. 04, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CDw90) (CD90 antigen).
DE Name=THY1;
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86016759; PubMed=2864690;
RA Seki T., Spurr N., Obata F., Goyert S., Goodfellow P., Silver J.;
RT "The human Thy-1 gene: structure and chromosomal location."
RL Proc. Natl. Acad. Sci. U.S.A. 82:6657-6661(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20403900; PubMed=10944468; DOI=10.1006/bbrc.2000.3282;
RA Ye Z., Connor J.R.;
RT "cDNA cloning by amplification of circularized first strand cDNAs reveals non-IRE-regulated iron-responsive mRNAs."
RL Biochem. Biophys. Res. Commun. 275:223-227(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Amygdala;
RG The German cDNA consortium;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain, and Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Raheyl J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Gichwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smailus D.E.,
Brunner A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RX NUCLEOTIDE SEQUENCE OF 1-55.
 RA MEDLINE=93240114; PubMed=7683034; DOI=10.1084/jem.177.5.1331;
 RA Craig W., Kay R., Cutler R.L., Lanadorp P.M.;
 RT "Expression of Thy-1 on human hematopoietic progenitor cells.";
 RL J. Exp. Med. 177:1331-1342(1993).
 CC -!- FUNCTION: May play a role in cell-cell or cell-ligand interactions
 CC during synaptogenesis and other events in the brain.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
 CC domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; M11749; AA61180.1; -; Genomic DNA.
 DR EMBL; AF261093; AAG13904.1; -; mRNA.
 DR EMBL; AL161958; CAB82306.1; -; mRNA.
 DR EMBL; BC005175; AAH05175.1; -; mRNA.
 DR EMBL; BC065559; AAH65559.1; -; mRNA.
 DR EMBL; S59749; AAB26353.2; -; mRNA.
 DR F1R; A02106; TDHU.
 DR F1R; T47130; T47130.
 DR Ensembl; ENSG00000154096; Homo sapiens.
 DR HGNC; HGNC:11801; THY1.
 DR H-InvDB; HIX0010195; -.
 DR MIM; 188230; -.
 DR GO; GO:0003887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005886; C:plasma membrane; NAS.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF000047; Ig; 1.
 DR SMART; SM00409; Ig; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR Glycoprotein; GPI-anchor; Immunoglobulin domain; Lipoprotein;
 KW Membrane; Signal; T-cell.
 FT SIGNAL 1 19
 FT CHAIN 20 130 Thy-1 membrane glycoprotein.
 FT PROPEP 131 161 Removed in mature form.
 FT DOMAIN 130 126 Ig-like V-type.
 FT LIPID 130 130 GPI-anchor amidated cysteine.
 FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 79 79 N-linked (GlcNAc...)
 FT CARBOHYD 119 119 N-linked (GlcNAc...)
 FT CARBOHYD 139 139 By similarity.
 FT DISULFID 28 130 By similarity.
 FT DISULFID 38 104 By similarity.
 FT CONFLICT 54 55 LT -> AP (in Ref. 5).
 FT CONFLICT 85 85 N -> H (in Ref. 1).
 FT CONFLICT 85 85
 SQ SEQUENCE 161 AA; 17935 MW; 2B6796DA8E7454B CRC64;
 SQ
 Query Match 66.7%; Score 630; DB 1; Length 161;
 Best Local Similarity 99.2%; Pred. No. 2.4e-47;
 Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 49 QKVTSLTACLVDSQLDCRHEHTSSPIQYEFSLTRTKKHVLFQVGPVPHYRSRTN 108
 DB 20 QKVTSLTACLVDSQLDCRHEHTSSPIQYEFSLTRTKKHVLFQVGPVPHYRSRTN 79
 QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRDLKVKCEGISLLAQN 168
 DB 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRDLKVKCEGISLLAQN 139
 QY 169 TS 170
 DB 140 TS 141
 RESULT 3
 THY1_MACMU
 ID THY1_MACMU STANDARD; PRT; 161 AA.
 AC O62643;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CD90) (CD90 antigen).
 DE
 GN Name=THY1;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Thymus;
 RA Margulies B.J., Clements J.E.;
 RT "Rhesus macaque CD90.";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May play a role in cell-cell or cell-ligand interactions
 CC during synaptogenesis and other events in the brain.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)

RESULT 2
 QSR508_PONPY
 ID QSR508_PONPY PRELIMINARY; PRT; 161 AA.
 AC QSR508;
 DT 01-FEB-2005 (TREMBlrel. 29, Created)
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE Hypothetical protein DKFZp459C1015.
 GN Name=DKFZp459C1015;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Cortex;
 RG The German cDNA Consortium;
 RA Bloeker H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C.,
 RA Osanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR861077; CAH93158.1; -; mRNA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF000047; Ig; 1.
 DR SMART; SM00406; Igv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Hypothetical protein; Immunoglobulin domain.
 SQ SEQUENCE 161 AA; 17963 MW; 2B6791DD8CB0401B CRC64;
 SQ
 Query Match 66.1%; Score 624; DB 2; Length 161;
 Best Local Similarity 97.5%; Pred. No. 8e-47;
 Matches 119; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 49 QKVTSLTACLVDSQLDCRHEHTSSPIQYEFSLTRTKKHVLFQVGPVPHYRSRTN 108
 DB 20 QKVTSLTACLVDSQLDCRHEHTSSPIQYEFSLTRTKKHVLFQVGPVPHYRSRTN 79
 QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRDLKVKCEGISLLAQN 168
 DB 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRDLKVKCEGISLLAQN 139
 QY 169 TS 170
 DB 140 TS 141
 RESULT 3
 THY1_MACMU
 ID THY1_MACMU STANDARD; PRT; 161 AA.
 AC O62643;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CD90) (CD90 antigen).
 DE
 GN Name=THY1;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Thymus;
 RA Margulies B.J., Clements J.E.;
 RT "Rhesus macaque CD90.";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May play a role in cell-cell or cell-ligand interactions
 CC during synaptogenesis and other events in the brain.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U93310; AAC05640.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Glycoprotein; GPI-anchor; Immunoglobulin domain; Lipoprotein;
KW Membrane; Signal; T-cell.
FT SIGNAL 1 19
FT CHAIN 20 130 Thy-1 membrane glycoprotein.
FT PROPEP 131 161 Removed in mature form.
FT DOMAIN 20 126 Ig-like V-type.
FT LIPID 130 130 GPI-anchor amidated cysteine.
FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 79 79 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 119 119 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 139 139 N-linked (GlcNAc...) (Potential).
FT DISULFID 28 130 By similarity.
FT DISULFID 38 104 By similarity.
SQ SEQUENCE 161 AA; 18011 MW; 326B135498BA401B CRC64;

Query Match 65.6%; Score 619; DB 1; Length 161;
Best Local Similarity 96.7%; Pred. No. 2.2e-46;
Matches 118; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVDSQSLRDCRHEHTSSPIQYFSLTRETKKHLFGTVGVPEHTYRSRTN 108
DB 20 QKVTSLTACLVDSQSLRDCRHEHTSSPIQYFSLTRETKKHLFGTVGVPEHTYRSRTN 79

QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRLDKLVKCEGISLLAQN 168
DB 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRLDKLVKCEGISLLAQN 139

QY 169 TS 170
DB 140 TS 141

RESULT 4
Q59GA0 HUMAN PRELIMINARY; PRT; 145 AA.
AC Q59GA0;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Thy-1 cell surface antigen variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Negase T., Kikuno F.R.;
RT "None Title.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB209209; BAD92446.1; -; mRNA.
FT NON TER 1 1
SQ SEQUENCE 145 AA; 15904 MW; 9DA4BC208DCD5766 CRC64;

Query Match 57.8%; Score 546; DB 2; Length 145;
Best Local Similarity 99.0%; Pred. No. 4.9e-40;
Matches 104; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 49 QKVTSLTACLVDSQSLRDCRHEHTSSPIQYFSLTRETKKHLFGTVGVPEHTYRSRTN 108
DB 36 QKVTSLTACLVDSQSLRDCRHEHTSSPIQYFSLTRETKKHLFGTVGVPEHTYRSRTN 95

QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRL 153
DB 96 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRL 140

RESULT 5
Q9WUR5 CAVPO PRELIMINARY; PRT; 161 AA.
ID Q9WUR5_CAVPO PRELIMINARY; PRT; 161 AA.
AC Q9WUR5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Thy-1 protein precursor.
DB Name=Thy-1;
GN Name=Thy-1;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Schaefer H., Burger R., Otto A., Bartels T.;
RT "Characterization and cloning of guinea pig Thy-1.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ238589; CAB44008.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 161 Thy-1 protein.
SQ SEQUENCE 161 AA; 17995 MW; 241461D901P80B1B CRC64;

Query Match 53.3%; Score 503; DB 2; Length 161;
Best Local Similarity 79.5%; Pred. No. 3.3e-36;
Matches 97; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVDSQSLRDCRHEHTSSPIQYFSLTRETKKHLFGTVGVPEHTYRSRTN 108
DB 20 QKVTSLTACLVDSQSLRDCRHEHTSSPIQYFSLTRETKKHLFGTVGVPEHTYRSRTN 79

QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRLDKLVKCEGISLLAQN 168
DB 80 LTSNYNIKVLYLANFTTKDEGTYTCALHSHGSHSPPISSQNVTVLRLDKLVKCEGISLLAQN 139

QY 169 TS 170
DB 140 TS 141

RESULT 6
THY1_RAT STANDARD; PRT; 161 AA.
ID THY1_RAT
AC P01830;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CD90 antigen).
DB Name=Thy1; Synonyms=Thy-1;
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
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RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=86005549; PubMed=2864289;
 RX Seki T., Chang H.-C., Moriuchi T., Denome R., Silver J.;
 RA "Thy-1: a hydrophobic transmembrane segment at the carboxyl
 terminus";
 RT Fed. Proc. 44:2865-2869(1985).
 RL Nature 301:80-82(1983).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 1-122.
 RX MEDLINE=83115223; PubMed=6130472;
 RA Moriuchi T., Chang H.-C., Denome R., Silver J.;
 RT "Thy-1 cDNA sequence suggests a novel regulatory mechanism.";
 RL Nature 313:485-487(1985).
 RN [3]
 RP NUCLEOTIDE SEQUENCE OF 20-161.
 RX MEDLINE=85111162; PubMed=2857477;
 RA Seki T., Moriuchi T., Chang H.-C., Denome R., Silver J.;
 RT "Structural organization of the rat thy-1 gene";
 RL Nature 313:485-487(1985).
 RN [4]
 RP NUCLEOTIDE SEQUENCE OF 20-161.
 RX MEDLINE=85051865; PubMed=6149956; DOI=10.1016/0014-5793(84)81250-8;
 RA Moriuchi T., Silver J.;
 RT "Rat Thy-1 antigen has a hydrophobic segment at the carboxyl
 terminus";
 RL FEBS Lett. 178:105-108(1984).
 RN [5]
 RP PROTEIN SEQUENCE OF 20-130.
 RX MEDLINE=82068190; PubMed=6118137;
 RA Campbell D.G., Gagnon J., Reid K.B.M., Williams A.F.;
 RT "Rat brain Thy-1 glycoprotein. The amino acid sequence, disulphide
 bonds and an unusual hydrophobic region.";
 RL Biochem. J. 195:15-30(1981).
 RN [6]
 RP STRUCTURE OF CARBOHYDRATES.
 RX MEDLINE=87275814; PubMed=2886334;
 RA Parekh R.B., Tee A.G.D., Dwek R.A., Williams A.F., Rademacher T.W.;
 RT "Tissue-specific N-glycosylation, site-specific oligosaccharide
 patterns and lentil lectin recognition of rat Thy-1.";
 RL EMBO J. 6:1233-1244(1987).
 CC -!- FUNCTION: May play a role in cell-cell or cell-ligand interactions
 during synaptogenesis and other events in the brain.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- TISSUE SPECIFICITY: Abundant in lymphoid tissues.
 CC -!- PTM: Glycosylation is tissue specific. Sialylation of N-glycans at
 Asn-93 in brain and at Asn-42, Asn-93 and Asn-117 in thymus.
 CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
 domain.
 CC -----
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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 DR EMBL; X03152; CAA26931.1; -; Genomic_DNA.
 DR EMBL; X03150; CAA26929.1; -; mRNA.
 DR EMBL; X02002; CAA26033.1; -; Genomic_DNA.
 DR EMBL; M18002; AAA42243.1; -; mRNA.
 DR EMBL; M10666; AAA42242.1; -; mRNA.
 DR FIR; B45909; TDRT.
 DR Ensembl; ENSRNOG0000006504; Rattus norvegicus.
 DR RGD; 3860; Thy1.
 DR GO; GO:0009986; C:cell surface; TAS.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00409; IG_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Direct protein sequencing; Glycoprotein; GPI-anchor;
 KW Immunoglobulin domain; Lipoprotein; Membrane;
 KW Pyroglutamate carboxylic acid; Sialic acid; Signal; T-cell.
 FT SIGNAL 1 19
 FT CHAIN 20 130 Thy-1 membrane glycoprotein.

FT PROPEP 131 161 Removed in mature form.
 FT DOMAIN 20 126 Ig-like V-type.
 FT MOD_RES 20 20 Pyroglutamate carboxylic acid.
 FT LIPID 130 130 GPI-anchor amidated cysteine.
 FT CARBOHYD 42 42 N-linked (GlcNAc...) (high mannose or
 complex); in thymus.
 FT CARBOHYD 42 42 N-linked (GlcNAc...) (high mannose); in
 brain.
 FT CARBOHYD 93 93 N-linked (GlcNAc...) (complex).
 FT CARBOHYD 117 117 N-linked (GlcNAc...) (complex); in
 thymus.
 FT CARBOHYD 117 117 N-linked (GlcNAc...) (high mannose or
 hybrid); in brain.
 FT DISULFID 28 130
 FT DISULFID 38 104
 FT CONFLICT 71 71
 SQ SEQUENCE 161 AA; 18172 MW; 3285748F3C2C5AB2 CRC64;
 E -> Q (in Ref. 1).
 Query Match 44.6%; Score 421; DB 1; Length 161;
 Best Local Similarity 67.2%; Pred. No. 5.1e-29;
 Matches 82; Conservative 15; Mismatches 25; Indels 0; Gaps 0;
 QY 49 QKVTSLTACLVDSQLRDLCHENTSSPIQYEFSLTRTKHVLFTGVPEHYRSRTN 108
 DB 20 QRVISLTACLVNQNLRLDCHENTNLPIQHEFSLTRKKHVLSTGLVPEHYRSRVN 79
 QY 109 FTSKYMVKVLSAPTSKDEGTTCALHSHSGSPPISSQNVTVLRDLKVKCGISLLAQN 168
 DB 80 LFSDFIRKVLTAFTTDEGDMCELRVSGQNPSTSSNKNTINVRDLKVKCGISLLVQN 139
 QY 169 TS 170
 DB 140 TS 141
 RESULT 7
 THY1_MOUSE
 ID THY1_MOUSE STANDARD; PRT; 162 AA.
 AC P01831;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CD90
 antigen).
 DE Name=Thy1; Synonyms=Thy-1;
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=85115360; PubMed=2857501;
 RA Seki T., Chang H.-C., Moriuchi T., Denome R., Ploegh H., Silver J.;
 RT "A hydrophobic transmembrane segment at the carboxyl terminus of thy-
 1.";
 RL Science 227:649-651(1985).
 RN [2]
 RP NUCLEOTIDE SEQUENCE (THY-1.2 ALLOTYPES).
 RX STRAIN=BALB/c;
 RX MEDLINE=86055760; PubMed=2866091;
 RA Giguere V., Isobe K.-I., Grosveld F.;
 RT "Structure of the murine Thy-1 gene";
 RL EMBO J. 4:2017-2024(1985).
 RN [3]
 RP NUCLEOTIDE SEQUENCE (THY-1.2 ALLOTYPES).
 RX MEDLINE=85216583; PubMed=2582427;
 RA Chang H.-C., Seki T., Moriuchi T., Silver J.;
 RT "Isolation and characterization of mouse Thy-1 genomic clones.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3819-3823(1985).
 RN [4]
 RP NUCLEOTIDE SEQUENCE (THY-1.2 ALLOTYPES).
 RX MEDLINE=86113437; PubMed=2868059;

RA Ingraham H.A., Lawless G.M., Evans G.A.;
 RT "The mouse Thy-1.2 glycoprotein gene: complete sequence and
 RT identification of an unusual promoter.";
 RL J. Immunol. 136:1482-1489(1986).
 RN [5]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toehiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.K., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RN PROTEIN SEQUENCES OF 20-131.
 RX MEDLINE=82159396; PubMed=6177036;
 RA Williams A.F., Gagnon J.;
 RT "Neuronal cell Thy-1 glycoprotein: homology with immunoglobulin.";
 RL Science 216:696-703(1982).
 CC -1- FUNCTION: May play a role in cell-cell or cell-ligand interactions
 CC during synaptogenesis and other events in the brain.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- POLYMORPHISM: There are two major alleles; Thy-1.2 and Thy-1.1.
 CC -1- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
 CC domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR ENBL; X03151; CAA26930.1; -; Genomic DNA.
 DR ENBL; X02771; CAA26548.1; -; Genomic DNA.
 DR ENBL; X02772; CAA26549.1; ALT SEQ; Genomic DNA.
 DR ENBL; X02773; CAA26550.1; ALT SEQ; Genomic DNA.
 DR ENBL; M10246; AAA40440.1; -; Genomic DNA.
 DR ENBL; M11160; AAA40441.1; -; Genomic DNA.
 DR ENBL; M12379; AAA40443.1; -; Genomic DNA.
 DR ENBL; BC054436; AAH54436.1; -; mRNA.
 DR PIR; A94278; TMS.
 DR Ensembl; ENSMUSG00000032011; Mus musculus.
 DR MGI; MGI:98747; Thy1.
 DR GO; GO:0009897; C:external side of plasma membrane; IDA.
 DR InterPro; IPR007110; Ig-like.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Direct protein sequencing; Glycoprotein; GPI-anchor;
 KW Immunoglobulin domain; Lipoprotein; Membrane; Polymorphism;
 KW Pyroglutamate carboxylic acid; Signal; T-cell.
 KW SIGNAL 1 19
 FT CHAIN 20 131 Thy-1 membrane glycoprotein.
 FT PROPEP 132 162 Removed in mature form.
 FT DOMAIN 20 127 Ig-like V-type.
 FT MOD_RES 20 20 Pyroglutamate carboxylic acid.
 FT LIPID 131 131 GPI-anchor amidated cysteine.
 FT CARBOHYD 42 42 N-linked (GlcNAc...).
 FT CARBOHYD 94 94 N-linked (GlcNAc...).
 FT CARBOHYD 118 118 N-linked (GlcNAc...).

FT DISULFID 28 131
 FT DISULFID 38 105
 FT VARIANT 108 108 Q -> R (in allele Thy-1.1).
 SQ SEQUENCE 162 AA; 18080 MW; 397BF7D3A9F2C77B CRC64;
 Query Match 43.1%; Score 406.5; DB 1; Length 162;
 Best Local Similarity 65.0%; Pred. No. 9.7e-28;
 Matches 80; Conservative 20; Mismatches 22; Indels 1; Gaps 1;
 QY 49 OKVTSITACLVDSLRDCRHE-NTSSSPIOYEFSLTRETKKHVLFGTVGVPEHTYRSRT 107
 DB 20 QKVTSLTACLVNQNLDCRHNNTKNSIQHEFSLTRKKRHVLSGLTGIPHTYRSRV 79
 QY 108 NPTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRDLKLVKCEGISLLAQ 167
 DB 80 TUSNQPIYKVLTLANFTTKDEGDFCELVSQGANPMSSNKSISVYRDLKLVKCGISLLVQ 139
 QY 168 NTS 170
 DB 140 NTS 142
 RESULT 8
 Q53YX2 MOUSE
 ID Q53YX2 MOUSE PRELIMINARY; PRT; 162 AA.
 AC Q53YX2
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE CD90.1.
 GN Name=Thy1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB;
 RA Delaître E., Jean L., Tron F., Boyer O.;
 RT "A single amino acid substitution confers CD90.1 (Thy1.1) allotype
 RT specificity.";
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY445633; AAR17087.1; -; mRNA.
 DR Ensembl; ENSMUSG00000032011; Mus musculus.
 DR MGI; MGI:98747; Thy1.
 DR GO; GO:0009897; C:external side of plasma membrane; IDA.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 162 AA; 18108 MW; 6978F4D3A9F2C530 CRC64;
 Query Match 43.1%; Score 406.5; DB 2; Length 162;
 Best Local Similarity 65.0%; Pred. No. 9.7e-28;
 Matches 80; Conservative 20; Mismatches 22; Indels 1; Gaps 1;
 QY 49 OKVTSITACLVDSLRDCRHE-NTSSSPIOYEFSLTRETKKHVLFGTVGVPEHTYRSRT 107
 DB 20 QKVTSLTACLVNQNLDCRHNNTKNSIQHEFSLTRKKRHVLSGLTGIPHTYRSRV 79
 QY 108 NPTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRDLKLVKCEGISLLAQ 167
 DB 80 TUSNQPIYKVLTLANFTTKDEGDFCELVSQGANPMSSNKSISVYRDLKLVKCGISLLVQ 139
 QY 168 NTS 170
 DB 140 NTS 142
 RESULT 9
 Q7T252_CHICK

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ID Q7T252_CHICK PRELIMINARY; PRT; 160 AA.
AC Q7T252;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE THY1.
GN Name=Thy1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14711516; DOI=10.1016/j.pep.2003.10.011;
RA Mehndiratta P., Walton W.J., Hare J.T., Fulido S., Parthasarathy G.,
RA Emmett M.R., Marshall A.G., Logan T.M.;
RT "Expression, purification, and characterization of avian Thy-1 from
RT Lec1 mammalian and Tn5 insect cells.";
RL Protein Expr. Purif. 33:274-287(2004).
DR EMBL; AY230132; AAP31241.1; -; mRNA.
DR Ensembl; ENSGALG0000006751; Gallus gallus.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; IG.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 160 AA; 18061 MW; 6DC39D8519540CE6 CRC64;

Query Match 33.9%; Score 320; DB 2; Length 160;
Best Local Similarity 48.4%; Pred. No. 3.7e-20;
Matches 59; Conservative 24; Mismatches 39; Indels 0; Gaps 0;

QY 49 QKVTSITACLVDSQSLRDCRHEHTSSPIQYFSLTRTKKHVLFQTVGVPHYRSRTN 108
Db 20 QMIRDLASCLGQSLRVDRCYENKTSNPLTYEFSLTRQ-QKHIIQSTISVSENVYRNAN 79

QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDLKVKCSGISLLAQN 168
Db 80 VTMHKNLVCLYLHSTTSDEGVYMCCELKATNDYTGNIKNITVTKLEKCKAGFSLLIQN 139

QY 169 TS 170
Db 140 TS 141

THY1_CHICK STANDARD; PRT; 160 AA.
AC Q07212;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thy-1 membrane glycoprotein precursor (Thy-1 antigen).
GN Name=Thy1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 43-55; 59-79 AND 81-101.
RC STRAIN=White leghorn; TISSUE=Brain;
RX MEDLINE=93061794; PubMed=1359371; DOI=10.1016/0169-328X(92)90180-J;
RA Dowling B.J., Gooley A.A., Gunning P., Cunningham A., Jeffrey P.L.;
RT "Molecular cloning and primary structure of the avian Thy-1
RT glycoprotein.";
RL Brain Res. Mol. Brain Res. 14:250-260(1992).
CC -!- FUNCTION: May play a role in cell-cell or cell-ligand interactions
CC during synaptogenesis and other events in the brain.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).

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CC -!- TISSUE SPECIFICITY: Forebrain, cerebellum and tectum.
CC -!- DEVELOPMENTAL STAGE: It is detected at embryonic day 4 (E4) in
CC forebrain and tectum. There is an increase in levels between E16
CC and the first few days post-hatch. During E19 to hatch a rapid
CC reduction in the levels is seen with a general increase in
CC expression in adulthood.
CC -!- PTM: The N-terminus is blocked.
CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
CC domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; S47368; AA111889.1; -; mRNA.
CC EMBL; L14924; AAC42216.1; -; mRNA.
CC PIR; A48975; A48975.
CC Ensembl; ENSGALG0000006751; Gallus gallus.
CC InterPro; IPR003599; IG.
CC SMART; SM00409; IG; 1.
CC Direct protein sequencing; Glycoprotein; GPI-anchor;
CC Immunoglobulin domain; Lipoprotein; Membrane;
CC Pyrrolidone carboxylic acid; Signal; T-cell.
KW Pyrrolidone carboxylic acid; Signal; T-cell.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 129 Thy-1 membrane glycoprotein.
FT PROPEP 130 160 Removed in mature form (By similarity).
FT MOD_RES 20 20 Pyrrolidone carboxylic acid (By
FT similarity).
FT LIPID 129 129 GPI-anchor amidated cysteine (By
FT similarity).
FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 78 78 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 118 118 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 138 138 N-linked (GlcNAc...) (Potential).
FT DISULFID 28 129 By similarity.
FT DISULFID 38 103 By similarity.
FT CONFLICT 76 76 R -> F (in Ref. 1; AA sequence).
FT CONFLICT 82 82 H -> I (in Ref. 1; AA sequence).
SQ SEQUENCE 160 AA; 18165 MW; E378D241CC2D4739 CRC64;

Query Match 32.4%; Score 305.5; DB 1; Length 160;
Best Local Similarity 48.4%; Pred. No. 6.9e-19;
Matches 59; Conservative 25; Mismatches 37; Indels 1; Gaps 1;

QY 49 QKVTSITACLVDSQSLRDCRHEHTSSPIQYFSLTRTKKHVLFQTVGVPHYRSRTN 108
Db 20 QMIRDLASCLGQSLRVDRCYENKTSNPLTYEFSLTRQ-QKHIIQSTISVSENVYRNAN 78

QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDLKVKCSGISLLAQN 168
Db 79 VTMHKNLVCLYLHSTTSDEGVYMCCELKATNDYTGNIKNITVTKLEKCKVRLSLIQN 138

QY 169 TS 170
Db 139 TS 140

RESULT 11
Q9XT67 CANFA
ID Q9XT67_CANFA PRELIMINARY; PRT; 60 AA.
AC Q9XT67;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Thy-1 (Fragment).
GN Name=Thy1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;

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RN RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99265967; PubMed=10331940; DOI=10.1006/geno.1999.5772;
RA Li R., Mignot E., Pakaco J., Kadotani H., Cantanese J., Zhao B.,
RA Lin X., Hinton L., Osterander E.A., Patterson D.F., de Jong P.J.,
RT "Construction and characterization of an eightfold redundant dog
RT genomic bacterial artificial chromosome library.;"
RL Genomics 58:9-17(1999).
RN (2)
RN RP NUCLEOTIDE SEQUENCE.
RA Kodatani H., Mignot E.;
RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103747; AD40573.1; -; Genomic DNA.
DR Ensembl; ENSCAG0000012021; Canis familiaris.
FT NON TER 1
FT NON TER 60
SQ SEQUENCE 60 AA; 6700 MW; 97AFAD948FD8D054 CRC64;
Query Match 25.8%; Score 244; DB 2; Length 60;
Best Local Similarity 78.3%; Pred. No. 5.3e-14;
Matches 47; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 94 GTGVPVHTYRSNTFTSKYHMKVLYLSAFTSKDECTYTCALHSHGSHSPISQNVTVLR 153
DB 1 GTGVPVHTYRSNTFTSKYHMKVLYLSAFTSKDECTYTCALHSHGSHSPISQNVTVLR 60
RESULT 12
O6PPFA_CAPHI PRELIMINARY; PRT; 45 AA.
AC O6PPFA;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Glucagon (Fragment).
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN (1)
RN NUCLEOTIDE SEQUENCE.
RA Ballaster M., Castello A., Ibanez E., Sanchez A., Folch J.M.;
RA Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY588290; AAT00451.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; Hormone 2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 1.
FT NON TER 1
FT NON TER 45
SQ SEQUENCE 45 AA; 5179 MW; B538A926E9447F80 CRC64;
Query Match 16.6%; Score 157; DB 2; Length 45;
Best Local Similarity 96.8%; Pred. No. 1.6e-06;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 HGRGTFTSDVSSYLEGQAAKEFIAWLVKRG 32
DB 13 HGRGTFTSDVSSYLEGQAAKEFIAWLVKRG 43
RESULT 13
GLUC SHEEP STANDARD; PRT; 176 AA.
ID _GLUC SHEEP
AC QBMJ25;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Glucagon precursor [Contains: Glucicentin; Glucicentin-related polypeptide
DE (GRPP); Oxyntomodulin (OXY) (OXM); Glucagon; Glucagon-like peptide 1
DE (GLP-1); Glucagon-like peptide 1(7-37) (GLP-1(7-37)); Glucagon-like
peptide 1(7-36) (GLP-1(7-36)); Glucagon-like peptide 2 (GLP-2)]
Name=GCG;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN (1)
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Pancreas;
RA Limesand S.W., Hay W.W. Jr.;
RA "Characterization of the endocrine pancreas in an ovine placental
RT insufficiency IUGR fetus.;"
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Glucagon plays a key role in glucose metabolism and
CC homeostasis. Regulates blood glucose by increasing gluconeogenesis
CC and decreasing glycolysis. A counterregulatory hormone of insulin,
CC raises plasma glucose levels in response to insulin-induced
CC hypoglycemia (By similarity).
CC -!- FUNCTION: GLP-1 is a potent stimulator of glucose-dependent
CC insulin release. play important roles on gastric motility and the
CC suppression of plasma glucagon levels. May be involved in the
CC suppression of satiety and stimulation of glucose disposal in
CC peripheral tissues, independent of the actions of insulin. Have
CC growth-promoting activities on intestinal epithelium. May also
CC regulate the hypothalamic pituitary axis (HPA) via effects on LH,
CC TSH, CRH, oxytocin, and vasopressin (By similarity).
CC -!- FUNCTION: GLP-2 stimulates intestinal growth and up-regulates
CC villus height in the small intestine, concomitant with increased
CC cell proliferation and decreased enterocyte apoptosis. The
CC gastrointestinal tract, from the stomach to the colon is the
CC principal target for GLP-2 action. Plays a key role in nutrient
CC homeostasis, enhancing nutrient assimilation through enhanced
CC gastrointestinal function, as well as increasing nutrient
CC disposal. Stimulates intestinal glucose transport and decreases
CC mucosal permeability (By similarity).
CC -!- FUNCTION: Oxyntomodulin significantly reduces food intake (By
CC similarity).
CC -!- FUNCTION: Glucicentin may modulate gastric acid secretion and
CC gastro-pyloro-duodenal activity.
CC -!- TISSUE SPECIFICITY: Glucagon is secreted in the A cells of the
CC islets of Langerhans. GLP-1, GLP-2, oxyntomodulin and glucicentin
CC are secreted from enteroendocrine cells throughout the
CC gastrointestinal tract. GLP1 and GLP2 are also secreted in
CC selected neurons in the brain.
CC -!- INDUCTION: Glucagon release is stimulated by hypoglycemia and
CC inhibited by hyperglycemia, insulin, and somatostatin. GLP-1 and
CC GLP-2 are induced in response to nutrient ingestion (By
CC similarity).
CC -!- PTM: Proglucagon is posttranslationally processed in a tissue-
CC specific manner in pancreatic A cells and intestinal L cells. In
CC pancreatic A cells, the major bioactive hormone is glucagon
CC cleaved by PCSK2/PC2. In the intestinal L cells PCSK1/PC1
CC liberates GLP-1, GLP-2, glucicentin and oxyntomodulin. GLP-1 is
CC further N-terminally truncated by posttranslational processing in
CC the intestinal L cells resulting in GLP-1(7-37) GLP-1(7-36)amide.
CC The C-terminal amidation is neither important for the metabolism
CC of GLP-1 nor for its effects on the endocrine pancreas (By
CC similarity).
CC -!- MISCELLANEOUS: GLP-2 does not have cleavage on a pair of basic
CC residues at C-terminus as in other mammals.
CC -!- SIMILARITY: Belongs to the glucagon family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF529185; AAM944409.1; -; mRNA.
DR
```

DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; Hormone 2; 3.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 3.
 DR PROSITE; PS00260; GLUCAGON; 4.
 KW Amidation; Cleavage on pair of basic residues; Glucagon family;
 KW Hormone; Signal.
 FT SIGNAL 1 20
 FT PEPTIDE 21 89
 FT PEPTIDE 21 50
 FT PEPTIDE 53 89
 FT PEPTIDE 53 81
 FT PROPEP 84 89
 FT PEPTIDE 92 128
 FT PEPTIDE 98 128
 FT PEPTIDE 98 127
 FT PROPEP 131 145
 FT PEPTIDE 146 >176
 FT SITE 52 53
 FT SITE 83 84
 FT SITE 91 92
 FT SITE 97 98
 FT SITE 130 131
 FT SITE 145 146
 FT MOD_RES 127 127
 FT NON_TER 176 176
 FT SEQUENCE 176 AA; 20336 MW; 13174039B6CE2B3 CRC64;
 SQ
 Query Match 16.6%; Score 157; DB 1; Length 176;
 Best Local Similarity 96.8%; Pred. No. 8.2e-06;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 HSEGTTSVSSYLEGQAQAKETAMLVKGRG 32
 DB 98 HAEGTFTSDVSSYLEGQAQAKETAMLVKGRG 128
 RESULT 14
 GLUC_BOVIN STANDARD; PRT; 180 AA.
 AC P01272;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Glucagon precursor [Contains: Glucicentin; Glucicentin-related polypeptide
 DE (GRPP); Oxyntomodulin (OXY) (OXM); Glucagon; Glucagon-like peptide 1
 DE (GLP-1); Glucagon-like peptide 1(7-37) (GLP-1(7-37)); Glucagon-like
 DE peptide 1(7-36) (GLP-1(7-36)); Glucagon-like peptide 2 (GLP-2)].
 GN Names-GCG;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=83299996; PubMed=6577439;
 RA Lopez L.C., Frazier M.L., Su C.-J., Kumar A., Saunders G.F.;
 RT "Mammalian pancreatic preproglucagon contains three glucagon-related
 RT peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:5485-5489(1983).
 RN [2]
 RP PROTEIN SEQUENCE OF 53-81.
 RX MEDLINE=71166445; PubMed=5102927;
 RA Bromer W.W., Boucher M.E., Koffenberger J.E. Jr.;
 RT "Amino acid sequence of bovine glucagon.";
 RL J. Biol. Chem. 246:2822-2827(1971).
 RN [3]

RP REVIEW.
 RA MEDLINE=22442611; PubMed=12554744; DOI=10.1210/me.2002-0306;
 RX Drucker D.J.;
 RT "Glucagon-like peptides: regulators of cell proliferation,
 RT differentiation, and apoptosis.";
 RL Mol. Endocrinol. 17:161-171(2003).
 RN [4]
 RP REVIEW.
 RX MEDLINE=22513095; PubMed=12626323; DOI=10.1152/ajpendo.00492.2002;
 RA Jiang G., Zhang B.B.;
 RT "Glucagon and regulation of glucose metabolism.";
 RL Am. J. Physiol. 284:E671-E678(2003).
 RN [5]
 RP REVIEW.
 RX PubMed=10322410;
 RA Drucker D.J.;
 RT "Glucagon-like peptide 2.";
 RL Trends Endocrinol. Metab. 10:153-156(1999).
 RN [6]
 RP REVIEW.
 RX MEDLINE=20073561; PubMed=10605628; DOI=10.1210/er.20.6.876;
 RA Kieffer T.J., Habener J.F.;
 RT "The glucagon-like peptides.";
 RL Endocr. Rev. 20:876-913(1999).
 RN [7]
 RP STRUCTURE BY NMR OF 53-81.
 RX MEDLINE=71166445; PubMed=6631957;
 RA Braun W., Wider G., Lee K.H., Wuehrich K.;
 RT "Conformation of glucagon in a lipid-water interphase by 1H nuclear
 RT magnetic resonance.";
 RL J. Mol. Biol. 169:921-948(1983).
 CC -!- FUNCTION: Glucagon plays a key role in glucose metabolism and
 CC homeostasis. Regulates blood glucose by increasing gluconeogenesis
 CC and decreasing glycolysis. A counterregulatory hormone of insulin,
 CC raises plasma glucose levels in response to insulin-induced
 CC hypoglycemia (By similarity).
 CC -!- FUNCTION: GLP-1 is a potent stimulator of glucose-dependent
 CC insulin release. Play important roles on gastric motility and the
 CC suppression of plasma glucagon levels. May be involved in the
 CC suppression of satiety and stimulation of glucose disposal in
 CC peripheral tissues, independent of the actions of insulin. Have
 CC growth-promoting activities on intestinal epithelium. May also
 CC regulate the hypothalamic pituitary axis (HPA) via effects on LH,
 CC TSH, CRH, oxytocin, and vasopressin secretion. Increases islet
 CC mass through stimulation of islet neogenesis and pancreatic beta
 CC cell proliferation (By similarity).
 CC -!- FUNCTION: GLP-2 stimulates intestinal growth and up-regulates
 CC villus height in the small intestine, concomitant with increased
 CC crypt cell proliferation and decreased enterocyte apoptosis. The
 CC gastrointestinal tract, from the stomach to the colon is the
 CC principal target for GLP-2 action. Plays a key role in nutrient
 CC homeostasis, enhancing nutrient assimilation through enhanced
 CC gastrointestinal function, as well as increasing nutrient
 CC disposal. Stimulates intestinal glucose transport and decreases
 CC mucosal permeability (By similarity).
 CC -!- FUNCTION: Oxyntomodulin significantly reduces food intake (By
 CC similarity).
 CC -!- FUNCTION: Glucicentin may modulate gastric acid secretion and
 CC gastro-pyloro-duodenal activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Glucagon is secreted in the A cells of the
 CC islets of Langerhans. GLP-1, GLP-2, oxyntomodulin and glucicentin
 CC are secreted from enteroendocrine cells throughout the
 CC gastrointestinal tract.
 CC -!- INDUCTION: Glucagon release is stimulated by hypoglycemia and
 CC inhibited by hyperglycemia, insulin, and somatostatin. GLP-1 and
 CC GLP-2 are induced in response to nutrient ingestion (By
 CC similarity).
 CC -!- PTM: Proglucagon is posttranslationally processed in a tissue-
 CC specific manner in pancreatic A cells and intestinal L cells. In
 CC pancreatic A cells, the major bioactive hormone is glucagon
 CC cleaved by PCSK2/PC2. In the intestinal L cells PCSK1/PC1
 CC liberates GLP-1, GLP-2, glucicentin and oxyntomodulin. GLP-1 is

further N-terminally truncated by posttranslational processing in the intestinal L cells resulting in GLP-1(7-37) GLP-1-(7-36)amide. The C-terminal amidation is neither important for the metabolism of GLP-1 nor for its effects on the endocrine pancreas (By similarity). Belongs to the glucagon family.

1- SIMILARITY: Belongs to the glucagon family.

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CC PDB; 1KK6; NMR; A=53-81.
 DR PDB; 1KK6; NMR; A=53-81.
 DR Pfam: PR00123; Hormone 2; 3.
 DR PRINTS; PR00275; GLUCAGON.
 DR PROSITE; PS00260; GLUCAGON; 4.
 KW 3D-structure; Amidation; Cleavage on pair of basic residues;
 KW Direct protein sequencing; Glucagon family; Hormone; Signal.
 FT SIGNAL 1 20
 FT PEPTIDE 21 89
 FT PEPTIDE 21 50
 FT PEPTIDE 53 89
 FT PEPTIDE 53 81
 FT PROPER 84 89
 FT PEPTIDE 92 128
 FT PEPTIDE 98 128
 FT PEPTIDE 98 127
 FT PEPTIDE 131 145
 FT PEPTIDE 146 178
 FT SITE 52 53
 FT SITE 83 84
 FT SITE 91 92
 FT SITE 97 98
 FT SITE 130 131
 FT SITE 145 146
 FT MOD_RES 127 127
 FT TURN 60 64
 FT TURN 74 74
 FT HELIX 75 78
 FT SEQUENCE 180 AA; 20944 MW; 8D9B4FF05B9F15FF CRC64;

Query Match 16.6%; Score 157; DB 1; Length 180;
 Best Local Similarity 96.8%; Pred. No. 8.4e-06;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 HSGGTFTSDVSSYLEGQAQKEFIATLVKGRG 32
 Db 98 HASEGTFTSDVSSYLEGQAQKEFIATLVKGRG 128

RESULT 15
 ID -GLUC CANFA STANDARD; PRT; 180 AA.
 AC P29794; Q95LG0;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 28-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Glucagon precursor [Contains: Glucicentin; Glucicentin-related polypeptide (GRP); Oxyntomodulin (OXY) (OXM); Glucagon; Glucagon-like peptide 1 (GLP-1); Glucagon-like peptide 1(7-37) (GLP-1(7-37)); Glucagon-like peptide 1(7-36) (GLP-1(7-36)); Glucagon-like peptide 2 (GLP-2)].
 GN Name=CCG;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Canidae;

CC Canis.
 OX NCBI_TaxID=9615;
 RN [1] NUCLEOTIDE SEQUENCE.
 RP TISSUE=Pancreas, and Stomach;
 RX PubMed=11916259;
 RA Irwin D.M.;
 RT "CDNA cloning of proglucagon from the stomach and pancreas of the dog.";
 RL DNA Seq. 12:253-260(2001).
 RN [2] PROTEIN SEQUENCE OF 21-89.
 RP TISSUE=ileum;
 RC MEDLINE=89185675; PubMed=3238052; DOI=10.1016/0167-0115(88)90230-3;
 RX Shinomura Y., Eng J., Yalow R.S.;
 RA "Immunoreactive glucagons purified from dog pancreas, stomach and ileum.";
 RL Regul. Pept. 23:299-308(1988).
 RN [3] PROCESSING BY PCSK1 AND PCSK2.
 RP PubMed=10499540; DOI=10.1210/en.140.10.4800;
 RA Damholt A.B., Buchan A.M., Holst J.J., Kofod H.;
 RT "Proglucagon processing profile in canine L cells expressing endogenous prohormone convertase 1/3 and prohormone convertase 2.";
 RL Endocrinology 140:4800-4808(1999).
 RN [4] REVIEW.
 RP PubMed=12554744; DOI=10.1210/me.2002-0306;
 RX Drucker D.J.;
 RA "Glucagon-like peptides: regulators of cell proliferation, differentiation, and apoptosis.";
 RL Mol. Endocrinol. 17:161-171(2003).
 RN [5] REVIEW.
 RP PubMed=12626323; DOI=10.1152/ajpendo.00492.2002;
 RX Jiang G., Zhang B.B.;
 RA "Glucagon and regulation of glucose metabolism.";
 RL Am. J. Physiol. 284:E671-E678(2003).
 RN [6] REVIEW.
 RP PubMed=10322410;
 RX Drucker D.J.;
 RA "Glucagon-like peptide 2.";
 RL Trends Endocrinol. Metab. 10:153-156(1999).
 RN [7] REVIEW.
 RP PubMed=10605628; DOI=10.1210/er.20.6.876;
 RX Kieffer T.J., Habener J.F.;
 RA "The glucagon-like peptides.";
 RL Endocr. Rev. 20:876-913(1999).
 CC -1- FUNCTION: Glucagon plays a key role in glucose metabolism and homeostasis. Regulates blood glucose by increasing gluconeogenesis and decreasing glycolysis. A counterregulatory hormone of insulin, raises plasma glucose levels in response to insulin-induced hypoglycemia (By similarity).
 CC -1- FUNCTION: GLP-1 is a potent stimulator of glucose-dependent insulin release. Play important roles on gastric motility and the suppression of plasma glucagon levels. May be involved in the peripheral tissues, independent of the actions of insulin. Have growth-promoting activities on intestinal epithelium. May also regulate the hypothalamic pituitary axis (HPA) via effects on LH, TSH, CRH, oxytocin, and vasopressin secretion. Increases islet mass through stimulation of islet neogenesis and pancreatic beta cell proliferation (By similarity).
 CC -1- FUNCTION: GLP-2 stimulates intestinal growth and up-regulates villus height in the small intestine, concomitant with increased crypt cell proliferation and decreased enterocyte apoptosis. The gastrointestinal tract, from the stomach to the colon is the principal target for GLP-2 action. Plays a key role in nutrient homeostasis, enhancing nutrient assimilation through enhanced gastrointestinal function, as well as increasing nutrient disposal. Stimulates intestinal glucose transport and decreases

Search completed: December 6, 2005, 10:41:51
Job time : 181.906 secs

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CC mucosal permeability (By similarity).
CC -!- FUNCTION: Oxyntomodulin significantly reduces food intake (By
CC similarity).
CC -!- FUNCTION: Glucagon may modulate gastric acid secretion and
CC gastro-pyloro-duodenal activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Glucagon is secreted in the A cells of the
CC islets of Langerhans. GLP-1, GLP-2, oxyntomodulin and glucagon
CC are secreted from enteroendocrine cells throughout the
CC gastrointestinal tract. GLP1 and GLP2 are also secreted in
CC selected neurons in the brain.
CC -!- INDUCTION: Glucagon release is stimulated by hypoglycemia and
CC inhibited by hyperglycemia, insulin, and somatostatin. GLP-1 and
CC GLP-2 are induced in response to nutrient ingestion (By
CC similarity).
CC -!- PTM: Proglucagon is posttranslationally processed in a tissue-
CC specific manner in pancreatic A cells and intestinal L cells. In
CC pancreatic A cells, the major bioactive hormone is glucagon
CC cleaved by PCSK2/PC2. In the intestinal L cells PCSK1/PC1
CC liberates GLP-1, GLP-2, glucagon and oxyntomodulin. GLP-1 is
CC further N-terminally truncated by posttranslational processing in
CC the intestinal L cells resulting in GLP-1(7-37) GLP-1-(7-36)amide.
CC The C-terminal amidation is neither important for the metabolism
CC of GLP-1 nor for its effects on the endocrine pancreas (By
CC similarity).
CC -!- SIMILARITY: Belongs to the glucagon family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF308439; AAL09425.1; -; mRNA.
CC PIR; A60318; GCDG69.
CC DR HSSP; P01274; 1GCN.
CC DR Ensembl; ENSCARG0000010414; Canis familiaris.
CC DR InterPro; IPR000532; Glucagon.
CC DR Pfam; PF00123; Hormone 2; 3.
CC DR PRINTS; PR00275; GLUCAGON.
CC DR SMART; SM00070; GLUCA; 3.
CC DR PROSITE; PS00260; GLUCAGON; 4.
CC KW Amidation; Cleavage on pair of basic residues;
CC KW Direct protein sequencing; Glucagon family; Hormone; Signal.
FT SIGNAL 1 20
FT PEPTIDE 21 89 Glucatin.
FT PEPTIDE 21 50 Glucatin-related polypeptide (By
FT similarity).
FT PEPTIDE 53 89 Oxyntomodulin (By similarity).
FT PEPTIDE 53 81 Glucagon (By similarity).
FT PROPEP 84 89 By similarity.
FT PEPTIDE 92 128 Glucagon-like peptide 1.
FT PEPTIDE 98 128 Glucagon-like peptide 1(7-37).
FT PEPTIDE 98 127 Glucagon-like peptide 1(7-36).
FT PROPEP 131 145 By similarity.
FT PEPTIDE 146 178 Glucagon-like peptide 2 (By similarity).
FT SITE 52 53 Cleavage (by PCSK2).
FT SITE 83 84 Cleavage (by PCSK1 and PCSK2).
FT SITE 91 92 Cleavage (by PCSK1).
FT SITE 97 98 Cleavage (by PCSK1).
FT SITE 130 131 Cleavage (by PCSK1).
FT SITE 145 146 Cleavage (by PCSK1).
FT MOD_RES 127 127 Arginine amide (G-128 provides amide
FT group) (By similarity).
SQ SEQUENCE 180 AA; 21115 MW; 80F66941AFC324FD CRC64;

Query Match 16.6%; Score 157; DB 1; Length 180;
Best Local Similarity 96.8%; Pred. No. 8.4e-06;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HGEFTFTSDVSSYLEGQAAKEFLAFLVKGKG 32
Db | ||||| ||||| ||||| ||||| ||||| |||||
98 HAEGTFTSDVSSYLEGQAAKEFLAFLVKGKG 128
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GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2005, 10:32:12 ; Search time 29.4355 Seconds
(without alignments)
575.296 Million cell updates/sec

Title: US-10-611-655-10
Perfect score: 944
Sequence: 1 MHGEGTFTSDVSSYLEGQAA.....VKCEGISLLAQTSHHHHH 176

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	637	67.5	161	1 TDHU	Thy-1 membrane gly
2	630	66.7	161	2 T47130	hypothetical prote
3	421	44.6	161	1 TDRT	Thy-1 membrane gly
4	406.5	43.1	162	1 TDMS	Thy-1 membrane gly
5	305.5	32.4	160	2 A48975	Thy-1 glycoprotein
6	157	16.6	158	1 GCPG	glucagon precursor
7	157	16.6	180	1 GCHY	glucagon precursor
8	157	16.6	180	1 GCHY	glucagon precursor
9	157	16.6	180	1 GCGP	glucagon precursor
10	157	16.6	180	1 GCHU	glucagon precursor
11	157	16.6	180	1 GCRT	glucagon precursor
12	157	16.6	180	1 GCRTDU	glucagon precursor
13	157	16.6	180	2 A57294	glucagon precursor
14	145	15.4	151	1 GCCH	glucagon precursor
15	145	15.4	206	2 I51301	proglucagon - chic
16	127	13.5	268	2 A56446	Ig heavy chain V r
17	125	13.2	101	1 GCFGB	glucagon precursor
18	122	12.9	30	2 C61125	glucagon-like pept
19	122	12.9	30	2 B61125	glucagon-like pept
20	122	12.9	122	1 GCAF2	Glucagon 2 precurs
21	114	12.1	66	2 I51093	glucagon - chinook
22	114	12.1	178	2 I51058	glucagon I precurs
23	113	12.0	63	1 GCIDC	glucagon precursor
24	112	11.9	72	1 GCGXA	glucagon precursor
25	112	11.9	411	2 I58156	Bra-3.2 - mouse
26	109.5	11.6	410	2 I38502	gene Bra-3b protei
27	109	11.5	60	1 GCQNC	glucagon precursor
28	109	11.5	178	2 I51057	glucagon II precur
29	107	11.3	30	2 S44473	glucagon-like pept

30	99.5	10.5	39	1 HWCH4G	exendin-4 - Gila m
31	99	10.5	87	1 GCFIS	glucagon precursor
32	98.5	10.4	2783	1 A41948	alpha-fetoprotein
33	96.5	10.2	124	1 GCAF	glucagon 1 precurs
34	96	10.2	29	2 S07211	glucagon - marbled
35	95.5	10.1	1022	2 T17406	developmental prot
36	95	10.1	31	2 S44472	glucagon G2 - Nort
37	95	10.1	877	2 T43449	hypothetical prote
38	94.5	10.0	160	2 H88114	protein F53C3.6 li
39	94	10.0	29	1 GCDP	glucagon - smaller
40	93	9.9	31	2 S44471	glucagon G1 - Nort
41	92.5	9.8	239	2 S49193	GCR 101 protein -
42	92.5	9.8	249	2 S41374	single chain Fv an
43	92	9.7	29	1 GCEN	glucagon - elephan
44	92	9.7	508	2 S59870	fork head domain p
45	92	9.7	1093	2 I38533	AF17 protein - hum

ALIGNMENTS

RESULT 1

TDHU

Thy-1 membrane glycoprotein precursor - human
N/Alternate names: Thy-1 antigen
C/Species: Homo sapiens (man)
C/Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C/Accession: A02106
R;Seki, T.; Spurr, N.; Obata, F.; Goyert, S.; Goodfellow, P.; Silver, J.
Proc. Natl. Acad. Sci. U.S.A. 82, 6657-6661, 1985
A/Title: The human Thy-1 gene: structure and chromosomal location.
A/Reference number: A02106; MUID:86016759; PMID:2864690
A/Accession: A02106
A/Molecule type: DNA
A/Residues: 1-161 <SEQ>
A/Cross-references: UNIPROT:P04216; UNIPARC:UPI0000049811; GB:M11749; NID:G339682; PIDN

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	630	66.7	161	2 T47130	hypothetical prote
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4	406.5	43.1	162	1 TDMS	Thy-1 membrane gly
5	305.5	32.4	160	2 A48975	Thy-1 glycoprotein
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7	157	16.6	180	1 GCHY	glucagon precursor
8	157	16.6	180	1 GCHY	glucagon precursor
9	157	16.6	180	1 GCGP	glucagon precursor
10	157	16.6	180	1 GCHU	glucagon precursor
11	157	16.6	180	1 GCRT	glucagon precursor
12	157	16.6	180	1 GCRTDU	glucagon precursor
13	157	16.6	180	2 A57294	glucagon precursor
14	145	15.4	151	1 GCCH	glucagon precursor
15	145	15.4	206	2 I51301	proglucagon - chic
16	127	13.5	268	2 A56446	Ig heavy chain V r
17	125	13.2	101	1 GCFGB	glucagon precursor
18	122	12.9	30	2 C61125	glucagon-like pept
19	122	12.9	30	2 B61125	glucagon-like pept
20	122	12.9	122	1 GCAF2	Glucagon 2 precurs
21	114	12.1	66	2 I51093	glucagon - chinook
22	114	12.1	178	2 I51058	glucagon I precurs
23	113	12.0	63	1 GCIDC	glucagon precursor
24	112	11.9	72	1 GCGXA	glucagon precursor
25	112	11.9	411	2 I58156	Bra-3.2 - mouse
26	109.5	11.6	410	2 I38502	gene Bra-3b protei
27	109	11.5	60	1 GCQNC	glucagon precursor
28	109	11.5	178	2 I51057	glucagon II precur
29	107	11.3	30	2 S44473	glucagon-like pept

RESULT 2

T47130

hypothetical protein DKFZp761B15121.1 - human
C/Species: Homo sapiens (man)
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C/Accession: T47130

Query Match 67.5%; Score 637; DB 1; Length 161;
Best Local Similarity 100.0%; Pred. No. 3.6e-48;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 QKVTSLTACLDVDSQSLDCHRENTSSSPQYSESLRRETKKHLFGTVGVPEHTYRSRTN 108
Db 20 QKVTSLTACLDVDSQSLDCHRENTSSSPQYSESLRRETKKHLFGTVGVPEHTYRSRTN 79

Qy 109 FTSKYHKVLYLSAFTSKDEGTYTCALHSHGHPPISSQNVTVLRDKLVKCEGISLLAQN 168
Db 80 FTSKYHKVLYLSAFTSKDEGTYTCALHSHGHPPISSQNVTVLRDKLVKCEGISLLAQN 139

Qy 169 TS 170
Db 140 TS 141

R;Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, March 2000

A;Reference number: Z24374
A;Accession: T47130
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-161 <AAA>
A;Cross-references: UNIPROT:P04216; UNIPARC:UPI0000136F1F; EMBL:AL161958
A;Experimental source: adult amygdala; clone DXFZp761B15121
C;Genetics:
A;Note: DXFZp761B15121.1
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 66.7%; Score 630; DB 2; Length 161;
Best Local Similarity 99.2%; Pred. No. 1.5e-47;
Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVDQSLRDCRHEHTSSSPIQYEFSLTRTKKHVLFGTVGVPHTYRSRTN 108
Db 20 QKVTSLTACLVDQSLRDCRHEHTSSSPIQYEFSLTRTKKHVLFGTVGVPHTYRSRTN 79

QY 109 FTSKYNMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRLDKLVKCGISLLAQN 168
Db 80 FTSKYNMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRLDKLVKCGISLLAQN 139

QY 169 TS 170
Db 140 TS 141

RESULT 3
TDPT
thy-1 membrane glycoprotein precursor - rat
N;Alternate names: thy-1 antigen
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jun-1981 #sequence revision 08-Feb-1996 #text change 09-Jul-2004
C;Accession: B45909; A45909; A25255; A21652; A90311; A93296; A02107
R;Seki, T.; Moriuchi, T.; Chang, H.C.; Denome, R.; Silver, J.
Nature 313, 485-487, 1985

A;Title: Structural organization of the rat thy-1 gene.
A;Reference number: A45909; MUID:85111162; PMID:2857477
A;Accession: B45909
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-161 <SEK>
A;Cross-references: UNIPROT:P01830; UNIPARC:UPI0000136F21; GB:X02002; NID:g57363; PIDN:G
A;Status: not compared with conceptual translation
A;Molecule type: mRNA

A;Residues: 20-161 <SE2>
A;Cross-references: UNIPARC:UPI0000170B3F
R;Seki, T.; Chang, H.C.; Moriuchi, T.; Denome, R.; Silver, J.
Fed. Proc. 44, 2865-2869, 1985
A;Title: Thy-1: a hydrophobic transmembrane segment at the carboxyl terminus.
A;Reference number: A25255; MUID:86005549; PMID:2864289

A;Accession: A25255
A;Molecule type: DNA
A;Residues: 1-70, 'Q', 72-161 <SE3>
A;Cross-references: UNIPARC:UPI0000170B3E; GB:X03152; NID:g57357; PIDN:CAA26931.1; PID:G
R;Moriuchi, T.; Silver, J.
FEBS Lett. 178, 105-107, 1984
A;Title: Rat Thy-1 antigen has a hydrophobic segment at the carboxyl terminus.
A;Reference number: A21652; MUID:85051865; PMID:6149956

A;Accession: A21652
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 20-161 <MOR>
A;Cross-references: UNIPARC:UPI0000170B3F; GB:X03150; GB:J00792; GB:X01445
R;Campbell, D.G.; Gagnon, J.; Reid, K.B.M.; Williams, A.F.
Biochem. J. 195, 15-30, 1981
A;Title: Rat brain Thy-1 glycoprotein. The amino acid sequence, disulphide bonds and an
A;Reference number: A90311; MUID:82068190; PMID:6118137
A;Accession: A90311

A;Molecule type: protein
A;Residues: 20-130 <CAM>
A;Cross-references: UNIPARC:UPI0000173743
A;Note: this sequence shows homologies with immunoglobulin domains
R;Moriuchi, T.; Chang, H.C.; Denome, R.; Silver, J.
Nature 301, 80-82, 1983
A;Title: Thy-1 cDNA sequence suggests a novel regulatory mechanism.
A;Reference number: A93296; MUID:83115223; PMID:6130472
A;Accession: A93296
A;Molecule type: mRNA
A;Residues: 1-122 <MO2>

A;Cross-references: UNIPARC:UPI0000173744
C;Comment: This glycoprotein is a major constituent of brain-cell membrane and is abunda
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein; membrane protein; pyroglutamic acid
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-130/Product: thy-1 membrane glycoprotein #status experimental <MAT>
F;31-106/Domain: immunoglobulin homology <IMM>
F;20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimer
F;28-130,38-104/Disulfide bonds: #status experimental
F;42,93,117/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 44.6%; Score 421; DB 1; Length 161;
Best Local Similarity 67.2%; Pred. No. 1.9e-29;
Matches 82; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVDQSLRDCRHEHTSSSPIQYEFSLTRTKKHVLFGTVGVPHTYRSRTN 108
Db 20 QKVTSLTACLVDQSLRDCRHEHTSSSPIQYEFSLTRTKKHVLFGTVGVPHTYRSRTN 79

QY 109 FTSKYNMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRLDKLVKCGISLLAQN 168
Db 80 FTSKYNMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRLDKLVKCGISLLAQN 139

QY 169 TS 170
Db 140 TS 141

RESULT 4

TOMS

Thy-1 membrane glycoprotein precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jul-1982 #sequence revision 28-May-1986 #text change 09-Jul-2004

C;Accession: A94278; A24647; A94265; I59028; I55957; A02108

R;Seki, T.; Chang, H.C.; Moriuchi, T.; Denome, R.; Floegh, H.; Silver, J.

Science 227, 649-651, 1985

A;Title: A hydrophobic transmembrane segment at the carboxyl terminus of Thy-1.

A;Reference number: A94278; MUID:85115360; PMID:2857501

A;Accession: A94278

A;Molecule type: DNA

A;Residues: 1-162 <SEK>

A;Cross-references: UNIPROT:P01831; UNIPARC:UPI00002395E; GB:M10246; NID:g202032; PIDN:

R;Giguere, V.; Isobe, K.I.; Grosveld, F.

EMBO J. 4, 2017-2024, 1985

A;Title: Structure of the murine Thy-1 gene.

A;Reference number: A24647; MUID:86055760; PMID:2866091

A;Contents: Thy-1.2 allotope

A;Accession: A24647

A;Molecule type: DNA

A;Residues: 1-162 <GIG>

A;Cross-references: UNIPARC:UPI000002395E

A;Experimental source: strain BALB/c

R;Williams, A.F.; Gagnon, J.

Science 216, 696-703, 1982

A;Title: Neuronal cell Thy-1 glycoprotein: homology with immunoglobulin.

A;Reference number: A94265; MUID:82199396; PMID:6177036

A;Accession: A94265

A;Molecule type: protein

A;Residues: 20-131 <WIL>

A;Cross-references: UNIPARC:UPI0000173745

A;Note: the Thy-1.1 sequence differs from that shown in having 108-Arg
R;Chang, H.

Proc. Natl. Acad. Sci. U.S.A. 82, 3819-3823, 1985
A;Title: Isolation and characterization of mouse Thy-1 genomic clones.
A;Reference number: I59028; MUID:85216583; PMID:2582427
A;Accession: I59028
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-162 <RES>
A;Cross-references: UNIPARC:UPI000002395E; GB:M11160; NID:G202034; PIDN:AAA40441.1; PID:
R;Ingraham, H.A.; Lawless, G.M.; Evans, G.A.
J. Immunol. 136, 1482-1489, 1986
A;Title: The mouse Thy-1.2 glycoprotein gene: Complete sequence and identification of an
A;Reference number: I55957; MUID:86113437; PMID:2868059
A;Accession: I55957
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-162 <RES>
A;Cross-references: UNIPARC:UPI000002395E; GB:M12379; NID:G202040; PIDN:AAA40443.1; PID:
C;Comment: The Thy-1.2 sequence is shown.
C;Genetics:
A;Map position: 9
A;Introns: 13/1; 126/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein; pyroglutamic acid; T-cell; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-162/Product: Thy-1 membrane glycoprotein #status predicted <MAT>
F;31-107/Domain: immunoglobulin homology <IMW>
F;143-162/Domain: transmembrane #status predicted <TMW>
F;20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
F;28-131.38-105/Disulfide bonds: #status experimental
F;42,94,118/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 43.1%; Score 406.5; DB 1; Length 162;
Best Local Similarity 65.0%; Pred. No. 3.4e-28;
Matches 80; Conservative 20; Mismatches 22; Indels 1; Gaps 1;

Qy 49 QKVTSLTACLVDSLRDCHRE-NTSSSPQYEFSTRETKKHVLFGTVCVPEHTYRSRT 107
Db 20 QKVTSLTACLVNQNLDRCHRENTDNSIQHEFSLTREKKHVLSTGLGIPHTYRSRV 79

Qy 108 NFTSKYHKVLYLSAFTSKDEGTYTCALHSHSGSPPISSONVTVLRLDKLVKCGISLLAQ 167
Db 80 TLSNQPIYKVLTLANFTTKDEGDFCELVQSGANPMSNKSISVYRDLKLVKCGISLLVQ 139

Qy 168 NTS 170
Db 140 NTS 142

RESULT 5
A48975
Thy-1 glycoprotein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48975
R;Dowsing, B.J.; Gooley, A.A.; Gunning, P.; Cunningham, A.; Jeffrey, P.L.
Brain Res. Mol. Brain Res. 14, 250-260, 1992
A;Title: Molecular cloning and primary structure of the avian Thy-1 glycoprotein.
A;Reference number: A48975; MUID:93061794; PMID:1359371
A;Accession: A48975
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-160 <DOM>
A;Cross-references: UNIPROT:Q07212; UNIPARC:UPI0000136P1D; GB:L14924; NID:G289826; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIN:117489, NCBIPI:117490)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein

Query Match 32.4%; Score 305.5; DB 2; Length 160;
Best Local Similarity 48.4%; Pred. No. 1.9e-19;
Matches 59; Conservative 25; Mismatches 37; Indels 1; Gaps 1;

Qy 49 QKVTSLTACLVDSLRDCHRENTSSSPQYEFSTRETKKHVLFGTVCVPEHTYRSRTN 108

Db 20 QMIRDSACLQSLRVDCRVENKTSNPLTYEFSLTRQ-QKHIIQSTISVSENVTNRAN 78

Qy 109 FTSKYHKVLYLSAFTSKDEGTYTCALHSHSGSPPISSONVTVLRLDKLVKCGISLLAQN 168
Db 79 VTMKRLVCLYLSHFTTSDEGYVMCELKATNDYTGQIKNTIVIKDLKCKVRLSLIQN 138

Qy 169 TS 170
Db 139 TS 140

RESULT 6
GCPG
glucagon precursor - pig (fragment)
N;Alternate names: glicentin; oxyntomodulin
N;Contains: glicentin-related peptide; glucagon; glucagon-37 (oxyntomodulin); glucagon-
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 17-Dec-1982 #sequence_revision 31-Mar-1993 #text_change 20-Mar-1998
C;Accession: A01540; A60312; A91781; B32614; A28064
R;Thim, L.; Moody, A.J.
Regul. Pept. 2, 139-150, 1981
A;Title: The primary structure of porcine glicentin (proglucagon).
A;Reference number: A94233; MUID:81248172; PMID:6894800
A;Accession: A01540
A;Molecule type: protein
A;Residues: 1-69 <TH1>
A;Cross-references: UNIPARC:UPI0000173500
R;Thim, L.; Moody, A.J.
Regul. Pept. Suppl. 2, S33, 1983
A;Title: Primary structure of a possible porcine proglucagon fragment.
A;Reference number: A60312
A;Accession: A60312
A;Molecule type: protein
A;Residues: 1-30 <TH2>
A;Cross-references: UNIPARC:UPI000002C9AC
A;Note: this peptide is co-secreted with glucagon from the pancreas
R;Bromer, W.W.; Sinn, L.G.; Behrens, O.K.
J. Am. Chem. Soc. 79, 2807-2810, 1957
A;Title: The amino acid sequence of glucagon. V. Location of amide groups, acid degrada
A;Reference number: A91781
A;Accession: A91781
A;Molecule type: protein
A;Residues: 33-61 <BRO>
A;Cross-references: UNIPARC:UPI000002C586
R;Orskov, C.; Bersani, M.; Johnsen, A.H.; Hojrup, P.; Holst, J.J.
J. Biol. Chem. 264, 12826-12829, 1989
A;Title: Complete sequences of glucagon-like peptide-1 from human and pig small intestine.
A;Reference number: A92732; MUID:89327238; PMID:2753890
A;Accession: B32614
A;Molecule type: protein
A;Cross-references: UNIPARC:UPI0000032E2A
R;Buhl, T.; Thim, L.; Kofod, H.; Orskov, C.; Harling, H.; Holst, J.J.
J. Biol. Chem. 263, 8621-8624, 1988
A;Title: Naturally occurring products of proglucagon 111-160 in the porcine and human s
A;Reference number: A28064; MUID:88243712; PMID:3379036
A;Accession: A28064
A;Molecule type: protein
A;Residues: 111-158 <BUH>
A;Cross-references: UNIPARC:UPI0000173501
C;Comment: X's represent missing amino acids, mostly basic, that are predicted to exist
C;Superfamily: glucagon
C;Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; interes
F;1-69/Product: glucagon-69 #status experimental <G69>
F;1-30/Region: glicentin-related peptide #status experimental
F;33-69/Product: glucagon-37 #status predicted <G37>
F;33-61/Product: glucagon #status experimental <GCN>
F;78-107/Product: glucagon-like peptide 1 #status experimental <GL1>
F;126-158/Product: glucagon-like peptide 2 #status experimental <GL2>
F;107/Modified site: amidated carboxyl end (Arg) (amide in mature form from following g

Query Match 16.6%; Score 157; DB 1; Length 158;
Best Local Similarity 96.8%; Pred. No. 1.4e-06;

A;Title: Structure of the human glucagon gene.
A;Reference number: A24377; MUID:86259053; PMID:3725587
A;Accession: A24377
A;Molecule type: DNA
A;Residues: 1-180 <WHI>
A;Cross-references: UNIPARC:UPI000012B832; GB:X03991
R;Bell, G.I.; Sanchez-Pescador, R.; Laybourn, P.J.; Najarian, R.C.
Nature 304, 368-371, 1983
A;Title: Exon duplication and divergence in the human preproglucagon gene.
A;Reference number: A44197; MUID:83271477; PMID:6877358
A;Accession: A44197
A;Molecule type: DNA
A;Residues: 1-179 <BEL>
A;Cross-references: UNIPARC:UPI000016A9A7; GB:V01515; NID:G31777; PIDN:CAA24759.1; PID:9
R;Drucker, D.J.; Asa, S.
J. Biol. Chem. 263, 13475-13478, 1988
A;Title: Glucagon gene expression in vertebrate brain.
A;Reference number: A30875; MUID:88330860; PMID:2901414
A;Accession: A30875
A;Molecule type: mRNA
A;Residues: 1-180 <DRU>
A;Cross-references: UNIPARC:UPI000012B832; GB:J04040; NID:G183269; PIDN:AAA52567.1; PID:
R;Orskov, C.; Bersani, M.; Johnsen, A.H.; Hojrup, P.; Holst, J.J.
J. Biol. Chem. 264, 12826-12829, 1989
A;Title: Complete sequences of glucagon-like peptide-1 from human and pig small intestine
A;Reference number: A92732; MUID:89327238; PMID:2753890
A;Accession: A32614
A;Molecule type: protein
A;Residues: 98-127 <ORS>
A;Cross-references: UNIPARC:UPI0000032E2A
R;Thomsen, J.; Kristiansen, K.; Brunfeldt, K.; Sundby, F.
FEBS Lett. 21, 315-319, 1972
A;Title: The amino acid sequence of human glucagon.
A;Reference number: A91373
A;Accession: A01541
A;Molecule type: protein
A;Residues: 53-81 <THO>
A;Cross-references: UNIPARC:UPI000002C586
R;Tsugita, A.; Takamoto, K.; Kamo, M.; Iwade, H.
Eur. J. Biochem. 206, 691-696, 1992
A;Title: C-terminal sequencing of protein. A novel partial acid hydrolysis and analysis
A;Reference number: S23188; MUID:92298996; PMID:1606956
A;Accession: S23309
A;Molecule type: protein
A;Residues: 53-81 <TSU>
A;Cross-references: UNIPARC:UPI000002C586
C;Comment: In pancreatic alpha-cells, proglucagon is processed to glucagon-like peptide 1, glucagon-
dulin. L cells, proglucagon is processed to truncated glucagon-like peptide 1, glucagon-
C;Genetics:
A;Gene: GDB:GCG
A;Cross-references: GDB:119265; OMIM:138030
A;Map position: 2q36-2q37
A;Introns: 31/2; 85/2; 131/2; 179/2
C;Superfamily: Glucagon
C;Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; intest
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-180/Product: proglucagon #status experimental <PGC>
F;21-89/Product: glucagon-like peptide 1 #status experimental <GLN>
F;53-89/Product: oxyntomodulin #status experimental <OXN>
F;53-81/Product: glucagon #status experimental <GCN>
F;92-178/Product: major proglucagon fragment #status experimental <MPGF>
F;92-127/Product: glucagon-like peptide 1 #status experimental <GLI>
F;98-127/Product: truncated glucagon-like peptide 1 #status experimental <TGL>
F;146-178/Product: glucagon-like peptide 2 #status predicted <GL2>
F;127/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl
Query Match 16.6%; Score 157; DB 1; Length 180;
Best Local Similarity 96.8%; Pred. No. 1.6e-06;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Caps 0;
QY 2 HGEFTFTSDVSSYLEGQAAKEFTIAWLKGRG 32

Db 98 HAEGTFTSDVSSYLEGQAAKEFTIAWLKGRG 128
RESULT 11
GCRTDU
Glucagon precursor - rat
N;Contains: glucicentin-related peptide; glucagon; glucagon-like peptide 1; glucagon-like
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1987 #sequence revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: A22655; A25190; A44198
R;Heinrich, G.; Gros, P.; Habener, J.F.
J. Biol. Chem. 259, 14082-14087, 1984
A;Title: Glucagon gene sequence: four of six exons encode separate functional domains o
A;Reference number: A22655; MUID:85054853; PMID:6094539
A;Accession: A22655
A;Molecule type: DNA
A;Residues: 1-180 <HEI>
A;Cross-references: UNIPROT:P06883; UNIPARC:UPI000002DB13; EMBL:K02809
A;Note: the authors translated the codon TTG for residue 10 as Glu and ACC for residue
R;Mojsov, S.; Heinrich, G.; Wilson, I.B.; Ravazzola, M.; Orci, L.; Habener, J.F.
J. Biol. Chem. 261, 11880-11889, 1986
A;Title: Preproglucagon gene expression in pancreas and intestine diversifies at the le
A;Reference number: A25190; MUID:86304324; PMID:3528148
A;Accession: A25190
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-180 <MOJ>
A;Cross-references: UNIPARC:UPI000002DB13
R;Heinrich, G.; Gros, P.; Lund, P.K.; Bentley, R.C.; Habener, J.F.
Endocrinology 115, 2176-2181, 1984
A;Title: Pre-proglucagon messenger ribonucleic acid: nucleotide and encoded amino acid
A;Reference number: A44198; MUID:85051023; PMID:6548696
A;Accession: A44198
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-180 <HE2>
A;Cross-references: UNIPARC:UPI000002DB13; GB:K02809; GB:K02810; GB:K02811; GB:K02812
C;Genetics:
A;Introns: 31/2; 85/2; 131/2; 179/2
C;Superfamily: glucagon
C;Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; pancr
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-180/Product: proglucagon #status predicted <PGC>
F;21-50/Region: glucicentin-related peptide #status predicted
F;53-81/Product: glucagon #status predicted <GCN>
F;98-127/Product: glucagon-like peptide 1 #status predicted <GL1>
F;146-180/Product: glucagon-like peptide 2 #status predicted <GL2>
F;127/Modified site: amidated carboxyl end (Arg) (amide in mature form from following g
Query Match 16.6%; Score 157; DB 1; Length 180;
Best Local Similarity 96.8%; Pred. No. 1.6e-06;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Caps 0;
QY 2 HGEFTFTSDVSSYLEGQAAKEFTIAWLKGRG 32
Db 98 HAEGTFTSDVSSYLEGQAAKEFTIAWLKGRG 128
RESULT 12
GCRTDU
Glucagon precursor - degu
N;Contains: glucicentin-related peptide; glucagon; glucagon-like peptide 1; glucagon-like
C;Species: Octodon degus (degu)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: C36118
R;Nishi, M.; Steiner, D.F.
Mol. Endocrinol. 4, 1192-1198, 1990
A;Title: Cloning of complementary DNAs encoding islet amyloid polypeptide, insulin, and
A;Reference number: A36118; MUID:91155952; PMID:2293024
A;Accession: C36118
A;Molecule type: mRNA
A;Residues: 1-180 <NIS>

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A;Reference number: A60836; MUID:88113418; PMID:2828209
A;Accession: A60836
A;Molecule type: protein
A;Residues: 55-83 <HUA>
A;Cross-references: UNIPARC:UPI000012B830
C;Superfamily: glucagon
C;Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; pancre
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-151/Product: proglucagon #status predicted <PGC>
F;55-83/Product: glucagon #status experimental <GCN>
F;118-147/Product: glucagon-like peptide 1 #status predicted <GLI>
F;147/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl
Query Match 15.4%; Score 145; DB 1; Length 151;
Beat Local Similarity 83.9%; Pred. No. 1.4e-05;
Matches 26; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 HEGTFTSDVSSYLEGQAAKEFIAMLVKGRG 32
| |||:||||:|||||
DB 118 HAEGTFTSDITSYLEGQAAKEFIAMLVNGRG 148

RESULT 15
151301
proglucagon - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51301
R;Irwin, D.M.; Wong, J.
Mol. Endocrinol. 9, 267-277, 1995
A;Title: Trout and chicken proglucagon: alternative splicing generates mRNA transcripts
A;Reference number: A55895; MUID:95295739; PMID:7776976
A;Accession: I51301
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-206 <IRW>
A;Cross-references: UNIPROT:P01277; UNIPARC:UPI000012B82E; GB:S78477; NID:G999386; PIDN
C;Superfamily: glucagon
C;Keywords: duplication

Query Match 15.4%; Score 145; DB 2; Length 206;
Beat Local Similarity 83.9%; Pred. No. 2e-05;
Matches 26; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 HEGTFTSDVSSYLEGQAAKEFIAMLVKGRG 32
| |||:||||:|||||
DB 118 HAEGTFTSDITSYLEGQAAKEFIAMLVNGRG 148

Search completed: December 6, 2005, 10:42:45
Job time : 30.4355 secs

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Result No.	Score	Query Match	Length	DB	ID	Description	
1	630	66.7	161	2	US-09-949-016-11168	Sequence 1168, A	
2	387	41.0	105	2	US-09-513-999C-4247	Sequence 4247, Ap	
3	174	18.4	176	1	US-08-835-231-18	Sequence 18, Appl	
4	174	18.4	176	2	US-09-108-661-18	Sequence 18, Appl	
5	163	17.3	31	1	US-09-209-799D-16	Sequence 16, Appl	
6	163	17.3	31	2	US-09-209-799D-16	Sequence 16, Appl	
7	163	17.3	31	2	US-09-614-847-113	Sequence 123, App	
8	163	17.3	31	2	US-09-997-792A-14	Sequence 14, Appl	
9	163	17.3	31	2	US-09-614-847-113	Sequence 147, App	
10	163	16.9	31	2	US-09-258-750-14	Sequence 142, App	
11	160	16.9	31	2	US-09-258-750-15	Sequence 14, Appl	
12	160	16.9	31	2	US-09-258-750-16	Sequence 15, Appl	
13	160	16.9	31	2	US-09-309-799D-28	Sequence 16, Appl	
14	160	16.9	31	2	US-09-398-111-14	Sequence 28, Appl	
15	160	16.9	31	2	US-09-398-111-15	Sequence 14, Appl	
16	160	16.9	31	2	US-09-398-111-16	Sequence 15, Appl	
17	160	16.9	31	2	US-09-987-792A-25	Sequence 16, Appl	
18	160	16.9	32	2	US-09-258-750-95	Sequence 25, Appl	
19	160	16.9	32	2	US-09-398-111-95	Sequence 95, Appl	
20	160	16.9	32	2	US-09-258-750-22	Sequence 22, Appl	
21	160	16.9	33	2	US-09-398-111-22	Sequence 22, Appl	
22	160	16.9	34	2	US-09-258-750-23	Sequence 23, Appl	
23	160	16.9	34	2	US-09-398-111-23	Sequence 23, Appl	
24	157	16.6	30	2	US-09-209-799D-15	Sequence 15, Appl	
25	157	16.6	30	2	US-09-614-847-87	Sequence 87, Appl	
26	157	16.6	30	2	US-09-614-847-112	Sequence 112, App	
27	157	16.6	30	2	US-09-614-847-113	Sequence 113, App	

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; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4247
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SIGNAL
; LOCATION: -19...-1
; OTHER INFORMATION: score 11.7
; OTHER INFORMATION: seq IALLTLVLQVSRG/QK
US-09-513-999C-4247

Query Match          41.0%; Score 387; DB 2; Length 105;
Best Local Similarity 87.1%; Pred. No. 1.8e-29;
Matches 74; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVPQSLRLDCRHEHTSSPIQYBFSLTRETKKHVLFGTVGVPEHTYRSRTN 108
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QKVTSLTACLVPQSLRLDCRHEHTSSPIQYBFSLTRETKKHVLFGTVGVPEHTYRSRTN 79

QY 109 FTSKYMVKVLYLSAFTSKDEGTYTC 133
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 FTSKYMVKVLYLSASLARTRALHVC 104

RESULT 3
US-08-835-231-18
; Sequence 18, Application US/08835231
; Patent No. 5861284
; GENERAL INFORMATION:
; APPLICANT: NISHIMURA, Osamu
; APPLICANT: KURIYAMA, Masato
; APPLICANT: KOYAMA, No. 5861284uyuki
; APPLICANT: FUKUDA, Tsunehiko
; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,231
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/350,709
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: 07/838,857
; FILING DATE: 18-FEB-1992
; APPLICATION NUMBER: JP 024841
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: JP 0271438
; FILING DATE: 18-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41614-FWC
; TELEPHONE: 617-523-3400
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 18:
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; REFERENCE/DOCKET NUMBER: 41614-FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 176 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-835-231-18

Query Match          18.4%; Score 174; DB 1; Length 176;
Best Local Similarity 76.6%; Pred. No. 6.4e-09;
Matches 36; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 1 MHGEFTFTSDVSSYLEGQAAXEFTIAWLVKRG----GGGGGGGGGEF 43
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MHAEGTFTSDVSSYLEGQAAXEFTIAWLVKRGCPEDGGSGAPPPGHF 47

RESULT 4
US-09-108-661-18
; Sequence 18, Application US/09108661
; Patent No. 6287806
; GENERAL INFORMATION:
; APPLICANT: NISHIMURA, Osamu
; APPLICANT: KURIYAMA, Masato
; APPLICANT: KOYAMA, No. 6287806uyuki
; APPLICANT: FUKUDA, Tsunehiko
; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/108,661
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/350,709
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: 07/838,857
; FILING DATE: 18-FEB-1992
; APPLICATION NUMBER: JP 024841
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: JP 0271438
; FILING DATE: 18-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41614-FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 18:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 176 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
;
US-09-108-661-18

Query Match      18.4%; Score 174; DB 2; Length 176;
Best Local Similarity 76.6%; Pred. No. 6.4e-09;
Matches 36; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 1 MHGEGTFTSDVSSYLEGQAAKEFIAWLKGRG---GGGSGGGGGRF 43
Db 1 MHGEGTFTSDVSSYLEGQAAKEFIAWLKGRGCPEDGGSGGPPGHF 47

RESULT 5
US-09-209-799D-16
; Sequence 16, Application US/09209799D
; Patent No. 6380357
; GENERAL INFORMATION:
; APPLICANT: Hermeling, Ronald
; APPLICANT: Hoffmann, James
; APPLICANT: Narasimhan, Chakravarthy
; TITLE OF INVENTION: GLUCAGON-LIKE PEPTIDE-1 CRYSTALS
; FILE REFERENCE: X-10242
; CURRENT APPLICATION NUMBER: US/09/209,799D
; CURRENT FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-209-799D-16

Query Match      17.3%; Score 163; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HGEFTFTSDVSSYLEGQAAKEFIAWLKGRG 32
Db 1 HGEFTFTSDVSSYLEGQAAKEFIAWLKGRG 31

RESULT 6
US-09-614-847-123
; Sequence 123, Application US/09614847
; Patent No. 6528486
; GENERAL INFORMATION:
; APPLICANT: Larsen, Bjarne Due
; APPLICANT: Mikkelsen, Jens Mollgaard
; APPLICANT: Neve, Soren
; TITLE OF INVENTION: NOVEL PEPTIDE AGONISTS OF GLP-1 ACTIVITY
; FILE REFERENCE: 55511(45487)
; CURRENT APPLICATION NUMBER: US/09/614,847
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/143,591
; PRIOR FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Lys (palmitoyl)
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Gly8-Glp-1(7-36)-Lys37 (palmitoyl) (Human)
US-09-614-847-123

Query Match      17.3%; Score 163; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.5e-09;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HGEFTFTSDVSSYLEGQAAKEFIAWLKGRG 32
Db 1 HGEFTFTSDVSSYLEGQAAKEFIAWLKGRG 31

RESULT 7
US-09-997-792A-14
; Sequence 14, Application US/09997792A
; Patent No. 655521
; GENERAL INFORMATION:
; APPLICANT: ELI LILLY and COMPANY
; TITLE OF INVENTION: Glucagon-Like Peptide-1 Crystals
; FILE REFERENCE: X-10242A
; CURRENT APPLICATION NUMBER: US/09/997,792A
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US 60/069,728
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-997-792A-14

Query Match      17.3%; Score 163; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HGEFTFTSDVSSYLEGQAAKEFIAWLKGRG 32
Db 1 HGEFTFTSDVSSYLEGQAAKEFIAWLKGRG 31

RESULT 8
US-09-614-847-147
; Sequence 147, Application US/09614847
; Patent No. 6528486
; GENERAL INFORMATION:
; APPLICANT: Larsen, Bjarne Due
; APPLICANT: Mikkelsen, Jens Mollgaard
; APPLICANT: Neve, Soren
; TITLE OF INVENTION: NOVEL PEPTIDE AGONISTS OF GLP-1 ACTIVITY
; FILE REFERENCE: 55511(45487)
; CURRENT APPLICATION NUMBER: US/09/614,847
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/143,591
; PRIOR FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 147
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (32)
; OTHER INFORMATION: Lys (palmitoyl)
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Gly8-Glp-1(7-36)-Lys37 (palmitoyl) (Human)
US-09-614-847-147

Query Match      17.3%; Score 163; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.5e-09;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HEGGFTSDVSSYLEGQAQKEFIAMLVKGRG 32
Db 1 HEGGFTSDVSSYLEGQAQKEFIAMLVKGRG 31

RESULT 9
US-09-614-847-122
; Sequence 122, Application US/09614847
; Patent No. 6528486
; GENERAL INFORMATION:
; APPLICANT: Larsen, Bjarne Due
; APPLICANT: Mikkelsen, Jens Mollgaard
; APPLICANT: Neve, Soren
; TITLE OF INVENTION: NOVEL PEPTIDE AGONISTS OF GLP-1 ACTIVITY
; FILE REFERENCE: 55511(45487)
; CURRENT APPLICATION NUMBER: US/09/614,847
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/143,591
; PRIOR FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 122
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: GLY8-GLP-1(7-37)-Lys6
US-09-614-847-122

Query Match 17.3%; Score 163; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HEGGFTSDVSSYLEGQAQKEFIAMLVKGRG 32
Db 1 HEGGFTSDVSSYLEGQAQKEFIAMLVKGRG 31

RESULT 10
US-09-258-750-14
; Sequence 14, Application US/09258750A
; Patent No. 6268343
; GENERAL INFORMATION:
; APPLICANT: KNUDSEN, LISELOTTE BJRERRE
; APPLICANT: HUUSFELDT, PER OLAF
; APPLICANT: NIELSEN, PER FRANKLIN
; TITLE OF INVENTION: GLP-1 DERIVATIVES
; FILE REFERENCE: 4790.500
; CURRENT APPLICATION NUMBER: US/09/258,750A
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 08/918,810
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: 60/035,905
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 60/036,226
; EARLIER FILING DATE: 1997-01-25
; EARLIER APPLICATION NUMBER: 60/036,255
; EARLIER FILING DATE: 1997-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutagen
US-09-258-750-14

Query Match 16.9%; Score 160; DB 2; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.6e-08;

Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HEGGFTSDVSSYLEGQAQKEFIAMLVKGRG 32
Db 1 HEGGFTSDVSSYLEGQAQKEFIAMLVKGRG 31

RESULT 11
US-09-258-750-15
; Sequence 15, Application US/09258750A
; Patent No. 6268343
; GENERAL INFORMATION:
; APPLICANT: KNUDSEN, LISELOTTE BJRERRE
; APPLICANT: HUUSFELDT, PER OLAF
; APPLICANT: NIELSEN, PER FRANKLIN
; TITLE OF INVENTION: GLP-1 DERIVATIVES
; FILE REFERENCE: 4790.500
; CURRENT APPLICATION NUMBER: US/09/258,750A
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 08/918,810
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: 60/035,905
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 60/036,226
; EARLIER FILING DATE: 1997-01-25
; EARLIER APPLICATION NUMBER: 60/036,255
; EARLIER FILING DATE: 1997-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutagen
US-09-258-750-15

Query Match 16.9%; Score 160; DB 2; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.6e-08;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HEGGFTSDVSSYLEGQAQKEFIAMLVKGRG 32
Db 1 HEGGFTSDVSSYLEGQAQKEFIAMLVKGRG 31

RESULT 12
US-09-258-750-16
; Sequence 16, Application US/09258750A
; Patent No. 6268343
; GENERAL INFORMATION:
; APPLICANT: KNUDSEN, LISELOTTE BJRERRE
; APPLICANT: HUUSFELDT, PER OLAF
; APPLICANT: NIELSEN, PER FRANKLIN
; TITLE OF INVENTION: GLP-1 DERIVATIVES
; FILE REFERENCE: 4790.500
; CURRENT APPLICATION NUMBER: US/09/258,750A
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 08/918,810
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: 60/035,905
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 60/036,226
; EARLIER FILING DATE: 1997-01-25
; EARLIER APPLICATION NUMBER: 60/036,255
; EARLIER FILING DATE: 1997-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutagen
US-09-258-750-16

Query Match 16.9%; Score 160; DB 2; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.6e-08;

OTHER INFORMATION: mutagen
US-09-258-750-16

Query Match 16.9%; Score 160; DB 2; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.6e-08;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HGEFTSDVSSYLEGQAAKEFTIAWLKGRG 32
|||||
Db 1 HGEFTSDVSSYLEGQAAKEFTIAWLKGRG 31

RESULT 13

US-09-209-799D-28
; Sequence 28, Application US/09209799D
; Patent No. 6380357
; GENERAL INFORMATION:
; APPLICANT: Hermeling, Ronald
; APPLICANT: Hoffmann, James
; APPLICANT: Narasimhan, Chakravarthy
; TITLE OF INVENTION: GLUCAGON-LIKE PEPTIDE-1 CRYSTALS
; FILE REFERENCE: X-10242
; CURRENT APPLICATION NUMBER: US/09/209,799D
; CURRENT FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 28
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-209-799D-28

Query Match 16.9%; Score 160; DB 2; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.6e-08;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HGEFTSDVSSYLEGQAAKEFTIAWLKGRG 32
|||||
Db 1 HGEFTSDVSSYLEGQAAKEFTIAWLKGRG 31

RESULT 14

US-09-398-111-14
; Sequence 14, Application US/09398111
; Patent No. 6458924
; GENERAL INFORMATION:
; APPLICANT: KNUDSEN, LISELOTTE BJERRE
; APPLICANT: HUISEFELDT, PER OLAF
; APPLICANT: NIELSEN, PER FRANKLIN
; TITLE OF INVENTION: GLP-1 DERIVATIVES
; FILE REFERENCE: 4790.500
; CURRENT APPLICATION NUMBER: US/09/398,111
; CURRENT FILING DATE: 1999-09-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/08/918,810A
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,905
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/036,226
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/036,255
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutagen
US-09-398-111-14

Query Match 16.9%; Score 160; DB 2; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.6e-08;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HGEFTSDVSSYLEGQAAKEFTIAWLKGRG 32
|||||
Db 1 HGEFTSDVSSYLEGQAAKEFTIAWLKGRG 31

RESULT 15

US-09-398-111-15
; Sequence 15, Application US/09398111
; Patent No. 6458924
; GENERAL INFORMATION:
; APPLICANT: KNUDSEN, LISELOTTE BJERRE
; APPLICANT: HUISEFELDT, PER OLAF
; APPLICANT: NIELSEN, PER FRANKLIN
; TITLE OF INVENTION: GLP-1 DERIVATIVES
; FILE REFERENCE: 4790.500
; CURRENT APPLICATION NUMBER: US/09/398,111
; CURRENT FILING DATE: 1999-09-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/08/918,810A
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,905
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/036,226
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/036,255
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutagen
US-09-398-111-15

Query Match 16.9%; Score 160; DB 2; Length 31;
Best Local Similarity 96.8%; Pred. No. 1.6e-08;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HGEFTSDVSSYLEGQAAKEFTIAWLKGRG 32
|||||
Db 1 HGEFTSDVSSYLEGQAAKEFTIAWLKGRG 31

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Job time : 41.0871 secs

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; SEQ ID NO 6
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric ThyOx carrier polypeptide containing
; OTHER INFORMATION: erythropoietin
US-10-611-655-6

Query Match      83.4%; Score 787; DB 5; Length 334;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 RGGGGSGGGGEGFGGGGSKVTSLTACLDVQSLRLDCRHSNTSSSPIQYEFSLTRTKKH 90
Db 189 RGGGGSGGGGEGFGGGGSKVTSLTACLDVQSLRLDCRHSNTSSSPIQYEFSLTRTKKH 248

QY 91 VLFGTGVPHTYRSRTNFTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNT 150
Db 249 VLFGTGVPHTYRSRTNFTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNT 308

QY 151 VLRLDKLVKCEGISLLAQTSHHHHH 176
Db 309 VLRLDKLVKCEGISLLAQTSHHHHH 334

RESULT 3
US-10-611-655-8
; Sequence 8, Application US/10611655
; Publication No. US2004026693A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides
; FILE REFERENCE: 66663-026
; CURRENT APPLICATION NUMBER: US/10/611,655
; CURRENT FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SuperEpo
US-10-611-655-8

Query Match      83.4%; Score 787; DB 5; Length 334;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 RGGGGSGGGGEGFGGGGSKVTSLTACLDVQSLRLDCRHSNTSSSPIQYEFSLTRTKKH 90
Db 189 RGGGGSGGGGEGFGGGGSKVTSLTACLDVQSLRLDCRHSNTSSSPIQYEFSLTRTKKH 248

QY 91 VLFGTGVPHTYRSRTNFTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNT 150
Db 249 VLFGTGVPHTYRSRTNFTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNT 308

QY 151 VLRLDKLVKCEGISLLAQTSHHHHH 176
Db 309 VLRLDKLVKCEGISLLAQTSHHHHH 334

RESULT 4
US-09-918-715-220
; Sequence 220, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
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; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 220
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-220

Query Match      67.5%; Score 637; DB 3; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 QKVTSLTACLDVQSLRLDCRHSNTSSSPIQYEFSLTRTKKHVLFGTVGVPHTYRSRTN 108
Db 20 QKVTSLTACLDVQSLRLDCRHSNTSSSPIQYEFSLTRTKKHVLFGTVGVPHTYRSRTN 79

QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNTVLRLDKLVKCEGISLLAQN 168
Db 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNTVLRLDKLVKCEGISLLAQN 139

QY 169 TS 170
Db 140 TS 141

RESULT 5
US-10-474-794-220
; Sequence 220, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-220

Query Match      67.5%; Score 637; DB 4; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 QKVTSLTACLDVQSLRLDCRHSNTSSSPIQYEFSLTRTKKHVLFGTVGVPHTYRSRTN 108
Db 20 QKVTSLTACLDVQSLRLDCRHSNTSSSPIQYEFSLTRTKKHVLFGTVGVPHTYRSRTN 79

QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNTVLRLDKLVKCEGISLLAQN 168
Db 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNTVLRLDKLVKCEGISLLAQN 139

QY 169 TS 170
Db 140 TS 141
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RESULT 6
US-10-979-159-220
; Sequence 220, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 220
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-979-159-220

Query Match 67.5%; Score 637; DB 5; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.2e-44; Indels 0; Gaps 0;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 49 QKVTSLTACLVDSLRDCHRENTSSPIQYFSLTRETCKHVLFGTVGVPHTYRSRTN 108
DB 20 QKVTSLTACLVDSLRDCHRENTSSPIQYFSLTRETCKHVLFGTVGVPHTYRSRTN 79
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCEGISLLAQN 168
DB 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCEGISLLAQN 139
QY 169 TS 170
DB 140 TS 141

RESULT 7
US-10-165-603-32
; Sequence 32, Application US/10165603
; Publication No. US20030021792A1
; GENERAL INFORMATION:
; APPLICANT: Roben, Paul W
; APPLICANT: Stevens, Anthony C.
; TITLE OF INVENTION: TISSUE-SPECIFIC ENDOTHELIAL MEMBRANE
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: TPTECH.001A
; CURRENT APPLICATION NUMBER: US/10/165,603
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/297,021
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/305,117
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-165-603-32

Query Match 66.7%; Score 630; DB 4; Length 161;
Best Local Similarity 99.2%; Pred. No. 4.5e-44;

Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 49 QKVTSLTACLVDSLRDCHRENTSSPIQYFSLTRETCKHVLFGTVGVPHTYRSRTN 108
DB 20 QKVTSLTACLVDSLRDCHRENTSSPIQYFSLTRETCKHVLFGTVGVPHTYRSRTN 79
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCEGISLLAQN 168
DB 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCEGISLLAQN 139
QY 169 TS 170
DB 140 TS 141

RESULT 8
US-10-794-899-66
; Sequence 66, Application US/10794899
; Publication No. US20040146516A1
; GENERAL INFORMATION:
; APPLICANT: Utah Ventures
; TITLE OF INVENTION: Lumen-Exposed Molecules and Methods Targeted Delivery
; FILE REFERENCE: 27110-715
; CURRENT APPLICATION NUMBER: US/10/794,899
; CURRENT FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-794-899-66

Query Match 66.7%; Score 630; DB 4; Length 161;
Best Local Similarity 99.2%; Pred. No. 4.5e-44; Indels 0; Gaps 0;
Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 49 QKVTSLTACLVDSLRDCHRENTSSPIQYFSLTRETCKHVLFGTVGVPHTYRSRTN 108
DB 20 QKVTSLTACLVDSLRDCHRENTSSPIQYFSLTRETCKHVLFGTVGVPHTYRSRTN 79
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCEGISLLAQN 168
DB 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCEGISLLAQN 139
QY 169 TS 170
DB 140 TS 141

RESULT 9
US-10-287-436A-449
; Sequence 449, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 449
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-449

Query Match 66.7%; Score 630; DB 5; Length 161;
Best Local Similarity 99.2%; Pred. No. 4.5e-44;

Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVDSRLDCRHSNTSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 108
|||:|||||
Db 20 QKVTSLTACLVDSRLDCRHSNTSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 79
|||:|||||
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTTCALHSHSGSPPISSQNVTVLRDCLKVCEGISLLAQN 168
|||:|||||
Db 80 FTSKYHMKVLYLSAFTSKDEGTYTTCALHSHSGSPPISSQNVTVLRDCLKVCEGISLLAQN 139
|||:|||||
QY 169 TS 170
|||
Db 140 TS 141

RESULT 10

US-10-287-436A-1149
; Sequence 1149, Application US/10287436A
; Publication No. US2005020421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1149
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-1149

Query Match 66.7%; Score 630; DB 5; Length 161;
Best Local Similarity 99.2%; Pred. No. 4.5e-44;
Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVDSRLDCRHSNTSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 108
|||:|||||
Db 20 QKVTSLTACLVDSRLDCRHSNTSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 79
|||:|||||
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTTCALHSHSGSPPISSQNVTVLRDCLKVCEGISLLAQN 168
|||:|||||
Db 80 FTSKYHMKVLYLSAFTSKDEGTYTTCALHSHSGSPPISSQNVTVLRDCLKVCEGISLLAQN 139
|||:|||||
QY 169 TS 170
|||
Db 140 TS 141

RESULT 11

US-09-925-301-1384
; Sequence 1384, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05982
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1384
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-925-301-1384

Query Match 66.7%; Score 630; DB 3; Length 165;
Best Local Similarity 99.2%; Pred. No. 4.6e-44;
Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVDSRLDCRHSNTSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 108
|||:|||||
Db 24 QKVTSLTACLVDSRLDCRHSNTSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 83
|||:|||||
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTTCALHSHSGSPPISSQNVTVLRDCLKVCEGISLLAQN 168
|||:|||||
Db 84 FTSKYHMKVLYLSAFTSKDEGTYTTCALHSHSGSPPISSQNVTVLRDCLKVCEGISLLAQN 143
|||:|||||
QY 169 TS 170
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Db 144 TS 145

RESULT 12

US-10-106-698-4624
; Sequence 4624, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 4624
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-4624

Query Match 66.7%; Score 630; DB 4; Length 165;
Best Local Similarity 99.2%; Pred. No. 4.6e-44;
Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVDSRLDCRHSNTSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 108
|||:|||||
Db 24 QKVTSLTACLVDSRLDCRHSNTSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 83
|||:|||||
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTTCALHSHSGSPPISSQNVTVLRDCLKVCEGISLLAQN 168
|||:|||||
Db 84 FTSKYHMKVLYLSAFTSKDEGTYTTCALHSHSGSPPISSQNVTVLRDCLKVCEGISLLAQN 143
|||:|||||
QY 169 TS 170
|||
Db 144 TS 145

RESULT 13

US-10-611-655-1
; Sequence 1, Application US/10611655
; Publication No. US20040266993A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides
; FILE REFERENCE: 66663-026
; CURRENT APPLICATION NUMBER: US/10/611,655
; CURRENT FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1

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; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-611-655-1

Query Match
Best Local Similarity 65.4%; Score 617.5; DB 5; Length 162;
Matches 121; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 49 QKVTSLTACLVDSLRDCHRENTSSPIQYEFSLTRETCKKHLFGTVGVPEHTYRSRTN 108
Db 20 QKVTSLTACLVDSLRDCHRENTSSPIQYEFSLTRETCKKHLFGTVGVPEHTYRSRTN 79

QY 109 FTSKYNKVLVLSAFTSKDEGTYTCALHSHGSHSPPI--SSQNVTVLRDKLKVCESILLAQ 167
Db 80 FTSKYNKVLVLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDKLKVCESILLAQ 139

QY 168 NTS 170
Db 140 NTS 142

RESULT 14
US-10-322-281-20
; Sequence 20, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-281-20

Query Match
Best Local Similarity 63.6%; Score 600; DB 4; Length 159;
Matches 118; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 49 QKVTSLTACLVDSLRDCHRENTSSPIQYEFSLTRETCKKHLFGTVGVPEHTYRSRTN 108
Db 20 QKVTSLTACLVDSLRDCHRENTSSPIQYEFSLTRETCKKHLFGTVGVPEH--YSRTN 77

QY 109 FTSKYNKVLVLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDKLKVCESILLAQ 168
Db 78 FTSKYNKVLVLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDKLKVCESILLAQ 137

QY 169 TS 170
Db 138 TS 139

RESULT 15
US-10-450-763-49897
; Sequence 49897, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
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; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 49897
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; LOCATION: (1)...(171)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-49897

Query Match
Best Local Similarity 44.9%; Score 424; DB 5; Length 171;
Matches 92; Conservative 9; Mismatches 21; Indels 6; Gaps 4;

QY 49 QKVTSLTACLVDSLRDCHRENTSSPIQYEFSLTRETCKKHLFGTVGVPEHTYRSRTN 108
Db 24 QKVTSLTACLVDSLRDCHRENTSSPSKIBFSLTRETCKKHLFGTVGVPEHTYRSRTN 83

QY 109 FTSKYHMK--VLVLSAFTSKDEGTYTCALHH--SGHSPPI--SSQNVTVL--RDKLKCEGI 162
Db 84 FTSKYNMEGFLTYSAFHXAATRGTLQVLQFHQFGALSPPFLSRNVTVVORTWVKCEGI 143

QY 163 SLLAQNTS 170
Db 144 SLLAQNTS 151

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Job time : 138.979 secs
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OM protein - protein search, using sw model

Run on: December 6, 2005, 10:37:02 ; Search time 7.35988 Seconds
(without alignments)
114.521 Million cell updates/sec

Title: US-10-611-655-10

Perfect score: 944

Sequence: 1 MHGEGTFTSDVSSYLEGQAA.....VKCEGISLAQNTSHHHHH 176

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:*
1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pap:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	160	16.9	70	US-10-997-061-28	Sequence 28, Appl
2	157	16.6	31	US-10-997-061-3	Sequence 3, Appl
3	156	16.5	277	US-10-997-061-11	Sequence 11, Appl
4	155	16.4	117	US-10-997-061-9	Sequence 9, Appl
5	155	16.4	122	US-10-997-061-31	Sequence 31, Appl
6	154	16.3	31	US-10-997-061-7	Sequence 7, Appl
7	152	16.1	119	US-10-997-061-13	Sequence 13, Appl
8	151	16.0	30	US-10-997-061-1	Sequence 1, Appl
9	151	16.0	31	US-10-997-061-4	Sequence 4, Appl
10	151	16.0	34	US-10-997-061-10	Sequence 10, Appl
11	151	16.0	34	US-10-997-061-12	Sequence 12, Appl
12	148	15.7	30	US-10-997-061-5	Sequence 5, Appl
13	148	15.7	31	US-10-997-061-8	Sequence 8, Appl
14	146	15.5	30	US-10-997-061-2	Sequence 2, Appl
15	144	15.3	259	US-11-054-515-1485	Sequence 1485, Ap
16	143	15.1	30	US-10-997-061-6	Sequence 6, Appl
17	138.5	14.7	256	US-11-054-515-1230	Sequence 1230, Ap
18	135	14.3	259	US-11-054-515-1552	Sequence 1552, Ap
19	134.5	14.2	249	US-11-054-515-1138	Sequence 1138, Ap
20	134	14.2	543	US-10-495-664-3	Sequence 3, Appl
21	131.5	13.9	252	US-11-054-515-1541	Sequence 1541, Ap
22	130.5	13.8	248	US-11-054-515-1254	Sequence 1254, Ap
23	130.5	13.8	618	US-10-512-184-48	Sequence 48, Appl
24	129.5	13.7	249	US-11-054-515-1856	Sequence 1856, Ap
25	129.5	13.7	252	US-11-054-515-1954	Sequence 1954, Ap

ALIGNMENTS

RESULT 1

US-10-997-061-28 256 7 US-11-054-515-1150 Sequence 1150, Ap
; Sequence 28, Application US/10997061 258 7 US-11-054-515-1038 Sequence 1038, Ap
; GENERAL INFORMATION: 246 7 US-11-054-515-1300 Sequence 1300, Ap
; APPLICANT: Wagner, Fred W. 241 7 US-11-054-515-2008 Sequence 2008, Ap
; APPLICANT: Luan, Peng 248 7 US-11-054-515-1037 Sequence 1037, Ap
; APPLICANT: Xia, Yuannan 254 7 US-11-054-515-1865 Sequence 1865, Ap
; APPLICANT: Rossard, Mary 250 7 US-11-054-515-1484 Sequence 1484, Ap
; APPLICANT: Holmquist, Barton H. 248 7 US-11-054-515-1976 Sequence 1976, Ap
; APPLICANT: Merrifield, Edwin H. 256 7 US-11-054-515-907 Sequence 907, App
; APPLICANT: Strydom, Daniel 248 7 US-11-054-515-1267 Sequence 1267, App
; APPLICANT: Restoragen Inc. 255 7 US-11-054-515-1483 Sequence 1483, Ap
; TITLE OF INVENTION: Method for Enzymatic Production of GLP-1 (7-36) Amide Peptides 248 7 US-11-054-515-1104 Sequence 1104, Ap
; FILE REFERENCE: 1627.003US1 250 7 US-11-054-515-859 Sequence 859, App
; CURRENT APPLICATION NUMBER: US/10/997,061 241 7 US-11-054-515-2032 Sequence 2032, Ap
; CURRENT FILING DATE: 2004-11-24 246 7 US-11-054-515-1702 Sequence 1702, Ap
; PRIOR APPLICATION NUMBER: PCT/US03/16469
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/383,214
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic peptide
US-10-997-061-28

Query Match 16.9%; Score 160; DB 6; Length 70;
Best Local Similarity 82.1%; Pred. No. 1.3e-08;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 HGBGTTSDVSSYLEGQAAKEFTIAWLKRGCGGGGGG 40
Db 4 HARGTTSDVSSYLEGQAAKEFTIAWLKRGGRHRAEG 42

RESULT 2

US-10-997-061-3
; Sequence 3, Application US/10997061
; Publication No. US20050260701A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, Fred W.
; APPLICANT: Luan, Peng
; APPLICANT: Xia, Yuannan

Db 2 MHAEGTFTSDVSSYLEGQAAKEFIAWLVKGR 32

RESULT 4

US-10-997-061-9

Sequence 9, Application US/10997061

Publication No. US20050260701A1

GENERAL INFORMATION:

APPLICANT: Wagner, Fred W.

APPLICANT: Luan, Peng

APPLICANT: Xia, Yuannan

APPLICANT: Bossard, Mary

APPLICANT: Holmquist, Barton

APPLICANT: Merrifield, Edwin H.

APPLICANT: Strydom, Daniel

APPLICANT: Restoragen Inc.

TITLE OF INVENTION: Method for Enzymatic Production of

FILE REFERENCE: 1627.003US1

CURRENT APPLICATION NUMBER: US/10/997,061

CURRENT FILING DATE: 2004-11-24

PRIOR APPLICATION NUMBER: PCT/US03/16469

PRIOR FILING DATE: 2003-05-23

```

; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; PRIOR APPLICATION NUMBER: US 00/393,213

```

```

; SEQ ID NO 3
;
; LENGTH: 117
;
; TYPE: PRT
;
; ORGANISM: Artificial Sequence

```

```

; OTHER INFORMATION: A synthetic peptide
;
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1
;
; OTHER INFORMATION: Xaa = T7-tag
US-10-397-061-9

Query Match          16.4%  Score 155;  DB 6;  Length 117;
Best Local Similarity 75.0%  Pred. No. 6.4e-08;
Matches 33;  Conservative 0;  Mismatches 9;  Indels 2;  Gaps 1;

Qy  2  HBGFTFTSDVSSYLEGQAAKEFIAWLVKGRG--GGGGSGGGGEF  43
      | | | | | | | | | | | | | | | | | | | | | |
Dd  9  HAEGTFTSDVSSYLEGQAAKEFIAWLVKGRAFLPGDGRHAEGTF  52
      | | | | | | | | | | | | | | | | | | | | | |

```

```

; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 00/363,214
;
; NUMBER OF SEQ ID NOS: 31
;
; SOFTWARE: FastSeq for Windows Version 4.0

```

```

; SEQ ID NO 31
; LENGTH: 122
; TYPE: PRT

```


US-10-997-061-2 ; Sequence 2, Application US/10997061
; Publication No. US20050260701A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, Fred W.
; APPLICANT: Luan, Peng

US-11-054-515-1485

```
Query Match      15.3%; Score 144; DB 7; Length 259;
Best Local Similarity 29.8%; Pred. No. 1.4e-06;
Matches 50; Conservative 21; Mismatches 68; Indels 30; Gaps 7;

QY 5 GTFTSDVSSYLEGQAAKEFIAM----LVKRGGGGGGGGEGFGGGGOKV----TSLTA 56
   |||  :|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 99 GTGYDILTGYMGSA---FDQWQGTTLVTVSSGGGGGGGGGGGSAQAVLTQPSLSA 155
   |||  :|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 57 -----CLVDQSLRLDCRH-----ENTSSSPIQYEFSLTRETAKHVLFGTVGVPEHTY 103
   |||  :|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 156 SPGASASLACTLRSDINLETSLRIYWFQKPGSPPRYLLRYQSDSNHL---DSGVPSRES 212
   |||  :|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 104 RSRTNFTSKYHMKVLYLSAFTSKDEGTYTCALHHSCHSPPISSQNVTVL 152
   |||  :|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 213 GSK---DASANAGILLISGVQSEDEADYHCMWHSGSVFGGGTKLTVL 258
   |||  :|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
```

Search completed: December 6, 2005, 10:48:05
Job time : 7.35888 sec

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 6, 2005, 10:32:12 ; Search time 164.348 Seconds
(without alignments)
470.529 Million cell updates/sec

Title: US-10-611-655-10

Perfect score: 944

Sequence: 1 MHGEGFTTSDVSSYLEGQAA.....VRCEGISLQAQNTSHHHHH 176

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 21.*

- 1: Geneseq1980s.*
- 2: Geneseq1980s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	944	100.0	176	9	Adw10192 Chimeric
2	787	83.4	334	9	Adw10190 Erythropo
3	787	83.4	334	9	Adw10188 Chimeric
4	637	67.5	161	5	Abb90744 Human Tum
5	637	67.5	161	6	Abu54451 Human Tum
6	630	66.7	161	7	Adp65208 Human Thy
7	630	66.7	161	8	Abu84755 Human can
8	630	66.7	161	9	Adz13572 Human can
9	630	66.7	161	9	Adz13574 Human can
10	630	66.7	161	9	Adz13570 Human can
11	630	66.7	165	3	Aab43939 Human can
12	630	66.7	165	4	Aag73850 Human col
13	617.5	65.4	162	9	Adw10183 Human Thy
14	604	64.0	368	2	Aay31789 Human Thy
15	600	63.6	119	2	Aay31787 Human Thy
16	546	57.8	150	8	Adk98542 Human imm
17	424	44.9	171	4	Abg19538 Novel hum
18	421	44.6	161	2	Aaw53480 Rat Thy-1
19	406.5	43.1	162	5	Abb90786 Mouse Tum
20	406.5	43.1	162	6	Abu54493 Mouse Tum
21	406.5	43.1	162	8	Abu84754 Murine ca
22	406.5	43.1	162	9	Adz13567 Murine ca
23	398	42.2	111	9	Adw10186 Thy-1 bas
24	389	41.2	368	2	Aay31788 Rat Thy-1

ALIGNMENTS

RESULT 1

ADW10192

ID ADW10192 standard; protein; 176 AA.

XX ADW10192;

XX DT 24-MAR-2005 (first entry)

XX Chimeric ThyOx carrier containing glucagon-like peptide 1.

XX non-immunoglobulin binding polypeptide; selective binding; ThyOx;

XX glucagon-like peptide 1; GLP-1.

XX Chimeric.

XX Synthetic.

XX US2004266993-A1.

XX 30-DEC-2004.

XX 30-JUN-2003; 2003US-00611655.

XX 30-JUN-2003; 2003US-00611655.

XX (EVAN/) EVANS G A.

XX Evans GA;

XX WPI; 2005-047648/05.

XX N-PSDB; ADW10191.

XX New chimeric non-immunoglobulin binding polypeptide comprises immunoglobulin-like domain containing scaffold and exhibits selective binding activity, for producing non-immunoglobulin binding polypeptides with selective binding activity.

XX Disclosure; SEQ ID NO 10; 45pp; English.

XX The invention relates to a novel chimeric non-immunoglobulin binding polypeptide. The polypeptide comprises an immunoglobulin-like domain containing scaffold with two or more solvent exposed loops containing a different complementarity-determining region (CDR) from a parent antibody inserted into each of the loops and exhibiting selective binding activity toward a ligand bound by the parent antibody. The invention further comprises: a chimeric ThyOx binding polypeptide, comprising one or more altered immunoglobulin-like domain loop regions of a ThyOx family polypeptide or at least one immunoglobulin-like domain containing

CC scaffold derived from a ThyOx family polypeptide, and a heterologous
CC binding polypeptide exhibiting selective binding activity toward a non-
CC ThyOx ligand; and a nucleic acid encoding the non-immunoglobulin or ThyOx
CC binding polypeptide above. The chimeric non-immunoglobulin binding
CC polypeptide is useful for producing non-immunoglobulin binding
CC polypeptides having selective binding activity toward a predetermined
CC molecule. This sequence represents a chimeric ThyOx carrier containing
CC glucagon-like peptide 1 of the invention.

XX Sequence 176 AA;

SQ Query Match 100.0%; Score 944; DB 9; Length 176;

Best Local Similarity 100.0%; Pred. No. 9.6e-85;

Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHCEGFTSDVSSYLEGQAKEFIAMLVKRGSGGGGGGGGGGGGKVTSLTACLVLD 60

DB 1 MHGEGFTSDVSSYLEGQAKEFIAMLVKRGSGGGGGGGGGGGGKVTSLTACLVLD 60

QY 61 QSLRLDCRHEHTSSSPIQEFSLTRETQKHVLFGTGVPEHTYRSRTNFTSKYHMKVLYL 120

DB 61 QSLRLDCRHEHTSSSPIQEFSLTRETQKHVLFGTGVPEHTYRSRTNFTSKYHMKVLYL 120

QY 121 SAFTSKDEGTYTTCALHSHGSPPISSQNTVLRDLKLVKCEGISLLAONTSHHHHH 176

DB 121 SAFTSKDEGTYTTCALHSHGSPPISSQNTVLRDLKLVKCEGISLLAONTSHHHHH 176

RESULT 2

ADW10190

ID ADW10190 standard; protein; 334 AA.

XX AC ADW10190;

XX DT 24-MAR-2005 (first entry)

XX DE Erythropoietin protein, named SuperEpo.

XX KW non-immunoglobulin binding polypeptide; selective binding; ThyOx;
KW erythropoietin; SuperEpo.

XX OS Chimeric.

XX OS Synthetic.

XX PN US2004266993-A1.

XX PD 30-DEC-2004.

XX PF 30-JUN-2003; 2003US-00611655.

XX PR 30-JUN-2003; 2003US-00611655.

XX PA (EVAN/) EVANS G A.

XX PI Evans GA;

XX DR WPI; 2005-047648/05.

XX DR N-PSDB; ADW10189.

XX PT New chimeric non-immunoglobulin binding polypeptide comprises
PT immunoglobulin-like domain containing scaffold and exhibits selective
PT binding activity, for producing non-immunoglobulin binding polypeptides
PT with selective binding activity.

XX PS Disclosure; SEQ ID NO 8; 45pp; English.

XX CC The invention relates to a novel chimeric non-immunoglobulin binding
CC polypeptide. The polypeptide comprises an immunoglobulin-like domain
CC containing scaffold with two or more solvent exposed loops containing a
CC different complementarity-determining region (CDR) from a parent antibody
CC inserted into each of the loops and exhibiting selective binding activity
CC toward a ligand bound by the parent antibody. The invention further
CC comprises a chimeric ThyOx binding polypeptide, comprising one or more

CC altered immunoglobulin-like domain loop regions of a ThyOx family
CC polypeptide or at least one immunoglobulin-like domain containing
CC scaffold derived from a ThyOx family polypeptide, and a heterologous
CC binding polypeptide exhibiting selective binding activity toward a non-
CC ThyOx ligand; and a nucleic acid encoding the non-immunoglobulin or ThyOx
CC binding polypeptide above. The chimeric non-immunoglobulin binding
CC polypeptide is useful for producing non-immunoglobulin binding
CC polypeptides having selective binding activity toward a predetermined
CC molecule. This sequence represents an erythropoietin protein, named
CC SuperEpo, of the invention.

XX Sequence 334 AA;

SQ Query Match 83.4%; Score 787; DB 9; Length 334;

Best Local Similarity 100.0%; Pred. No. 6.5e-69;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 RGGGGGGGGGGGFGGGGSGKVTSLTACLVDSRLDCRHEHTSSSPIQEFSLTRETQKH 90

DB 189 RGGGGGGGGGGGFGGGGSGKVTSLTACLVDSRLDCRHEHTSSSPIQEFSLTRETQKH 248

QY 91 VLFGTGVPEHTYRSRTNFTSKYHMKVLYLSAFTSKDEGTYTTCALHSHGSPPISSQNT 150

DB 249 VLFGTGVPEHTYRSRTNFTSKYHMKVLYLSAFTSKDEGTYTTCALHSHGSPPISSQNT 308

QY 151 VLRLDKLVKCEGISLLAONTSHHHHH 176

DB 309 VLRLDKLVKCEGISLLAONTSHHHHH 334

RESULT 3

ADW10188

ID ADW10188 standard; protein; 334 AA.

XX AC ADW10188;

XX DT 24-MAR-2005 (first entry)

XX DE Chimeric ThyOx carrier containing erythropoietin.

XX KW non-immunoglobulin binding polypeptide; selective binding; ThyOx;
KW erythropoietin.

XX OS Chimeric.

XX OS Synthetic.

XX PN US2004266993-A1.

XX PD 30-DEC-2004.

XX PF 30-JUN-2003; 2003US-00611655.

XX PR 30-JUN-2003; 2003US-00611655.

XX PA (EVAN/) EVANS G A.

XX PI Evans GA;

XX DR WPI; 2005-047648/05.

XX DR N-PSDB; ADW10187.

XX PT New chimeric non-immunoglobulin binding polypeptide comprises
PT immunoglobulin-like domain containing scaffold and exhibits selective
PT binding activity, for producing non-immunoglobulin binding polypeptides
PT with selective binding activity.

XX PS Disclosure; SEQ ID NO 6; 45pp; English.

XX CC The invention relates to a novel chimeric non-immunoglobulin binding
CC polypeptide. The polypeptide comprises an immunoglobulin-like domain
CC containing scaffold with two or more solvent exposed loops containing a
CC different complementarity-determining region (CDR) from a parent antibody
CC inserted into each of the loops and exhibiting selective binding activity

toward a ligand bound by the parent antibody. The invention further comprises: a chimeric ThyOx binding polypeptide, comprising one or more altered immunoglobulin-like domain loop regions of a ThyOx family polypeptide or at least one immunoglobulin-like domain containing scaffold derived from a ThyOx family polypeptide, and a heterologous binding polypeptide exhibiting selective binding activity toward a non-ThyOx ligand; and a nucleic acid encoding the non-immunoglobulin or ThyOx binding polypeptide above. The chimeric non-immunoglobulin binding polypeptide is useful for producing non-immunoglobulin binding polypeptides having selective binding activity toward a predetermined molecule. This sequence represents a chimeric ThyOx carrier containing erythropoietin of the invention.

```

SQ Sequence 334 AA;
Query Match      83.4%; Score 787; DB 9; Length 334;
Best Local Similarity 100.0%; Pred. No. 6.5e-69;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY  31  RGGGGGGGGGFFGGGSGKVTSLTACLVDSLRLDCRHENTSSSPIQYEFSLTRETKKH  90
      |||||
Db   189  RGGGGGGGGGFFGGGSGKVTSLTACLVDSLRLDCRHENTSSSPIQYEFSLTRETKKH  248

QY  91  VLFGTGVPEHTYRSRTNFTSKYHKMKVLYLSAFTSKDEGTYTCALHHSCHSPPISSQNT  150
      |||||
Db   249  VLFGTGVPEHTYRSRTNFTSKYHKMKVLYLSAFTSKDEGTYTCALHHSCHSPPISSQNT  308

QY  151  VL RDKL VKCEGISLLAONTSHHHHHH  176
      |||||
Db   309  VL RDKL VKCEGISLLAONTSHHHHHH  334

```

The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL920075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers (PEM) ABL91903-ABL91995

Query Match	67.5%; Score 637; DB 5; Length 161;
Best Local Similarity	100.0%; Pred. No. 1.6e-54;
Matches 122; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	49 QKVTSLTACLVDDQSLRDCRHENTSSSPIOYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 108
Db	20 QKVTSLTACLVDDQSLRDCRHENTSSSPIOYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 79
QY	109 FTSKYHMKVLYLSAFTSKDGGTYTCALHHSGHSPPISSQNVTVLKLVKCEGISLLAQN 168
Db	80 FTSKYHMKVLYLSAFTSKDGGTYTCALHHSGHSPPISSQNVTVLKLVKCEGISLLAQN 139
QY	169 TS 170
Db	140 TS 141
RESULT 5	
ABU54451	
ID	ABU54451 standard; protein; 161 AA.
XX	XX ABU54451;
XX	12-MAR-2003 (first entry)
XX	Human tumour endothelial marker TEM 13.
XX	Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
KW	Tumour endothelial marker; normal endothelial marker; PEM;
KW	pan-endothelial marker; polycystic kidney disease; psoriasis;
KW	diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
KW	neovascularization; immune response; cytostatic; antidiabetic;
KW	ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
XX	
OS	Homo sapiens.
XX	
XX	WO200283874-A2.
XX	
XX	24-OCT-2002.
PD	
XX	
XX	10-APR-2002; 2002WO-US008253.
PF	
XX	
XX	11-APR-2001; 2001US-0282850P.
PR	
PR	06-FEB-2002; 2002US-0354262P.
XX	
XX	(UUYO) UNIV JOHNS HOPKINS.
PA	
XX	
PI	Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
XX	
XX	WPI; 2003-093016/08.
XX	N-PSDB; ABX72023.
DR	
XX	
XX	New purified human transmembrane protein, designated as tumor endothelial
PT	marker (TEM) 3, useful for detecting, diagnosing or treating tumors, or
PT	polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
PT	psoriasis.
XX	
PT	

PS Disclosure; Page 206-207; 374pp; English.

XX The present invention relates to a novel method for the isolation of

CC endothelial cells (ECs), and the identification of genes expressed in

CC normal and tumour ECs. Tumour endothelial marker (TEM), normal

CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are

CC identified in human ECs. The human EC marker proteins and the

CC polynucleotide sequences encoding them are useful for detecting,

CC diagnosing or treating tumours as well as polycystic kidney disease,

CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also

CC useful for inhibiting neoangiogenesis or tumour angiogenesis, for

CC inducing an immune response to tumour endothelial cells in a patient, or

CC for identifying candidate drugs for treating tumours. The present

CC sequence represents a human TEM or NEM protein of the invention

XX

SQ Sequence 161 AA;

Query Match 67.5%; Score 637; DB 6; Length 161;

Best Local Similarity 100.0%; Pred. No. 1.6e-54;

Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVDSRLDCRHNNTSSPIQYEFSLTRETCKHVLFGTVGVPHTYRSRTN 108

DB 20 QKVTSLTACLVDSRLDCRHNNTSSPIQYEFSLTRETCKHVLFGTVGVPHTYRSRTN 79

QY 109 FTSKHYMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSONVTVLRDKLVKCGISLLAQN 168

DB 80 FTSKHYMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSONVTVLRDKLVKCGISLLAQN 139

QY 169 TS 170

DB 140 TS 141

RESULT 6

ADP65208

ID ADP65208 standard; protein; 161 AA.

AC ADP65208;

XX

XX 12-AUG-2004 (first entry)

XX Human Thy-1 cell surface antigen, Thy-1 T-cell antigen.

DE

DE autoimmune disease; arthritis; gene expression analysis;

KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;

KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;

KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;

KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;

KW immune; human.

XX

OS Homo sapiens.

XX

XX WO2003072827-A1.

XX

XX 04-SEP-2003.

XX

XX 31-OCT-2002; 2002WO-US035433.

XX

XX 31-OCT-2001; 2001US-0336220P.

XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX

PI Hirsch R, Thorton SL;

XX

DR WPI; 2003-712740/67.

DR GENBANK; NP_006279.

XX

XX Diagnosing and analyzing autoimmune disease using gene expression

PT profiles and microarray technology, useful for diagnosing and treating

PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and

PT gout.

XX

PS Disclosure; Page; 56pp; English.

XX The invention relates to a novel method for diagnosing and analysing

CC autoimmune disease or arthritides. The method comprises obtaining a

CC patient sample containing mRNA, analysing gene expression using the mRNA

CC that results in a gene expression signature of the mRNA, and using that

CC gene expression signature to diagnose or analyse the autoimmune disease

CC or arthritides in the patient, where gene expression of at least 60% of

CC the genes correlates with that of the gene signature. The invention

CC further comprises: a treatment of rheumatoid arthritis; identification of

CC genes for targeting in the treatment of rheumatoid arthritis in a mammal

CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an

CC array or gene chip, specific for rheumatoid arthritis; diagnosis or

CC analyses of autoimmune disease or rheumatoid arthritis; screening the

CC efficacy of a candidate drug in vitro for the treatment of collagen-

CC induced arthritis; and reducing the symptoms associated with collagen-

CC induced arthritis. The compositions of the invention have the following

CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,

CC antigout, antiinflammatory, dermatological, and immunomodulatory. The

CC methods and compositions of the present invention are useful for

CC diagnosing and treating autoimmune disease or arthritides, such as

CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,

CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an

CC immune disease caused by an infectious agent. This sequence represents a

CC protein sequence relating to the genes used in the analysis and treatment

CC of autoimmune diseases or arthritides. Note: This sequence is not shown

CC in the specification. It has been supplied in an electronic format from

CC WIPO.

XX

SQ Sequence 161 AA;

Query Match 66.7%; Score 630; DB 7; Length 161;

Best Local Similarity 99.2%; Pred. No. 7.9e-54;

Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVDSRLDCRHNNTSSPIQYEFSLTRETCKHVLFGTVGVPHTYRSRTN 108

DB 20 QKVTSLTACLVDSRLDCRHNNTSSPIQYEFSLTRETCKHVLFGTVGVPHTYRSRTN 79

QY 109 FTSKHYMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSONVTVLRDKLVKCGISLLAQN 168

DB 80 FTSKHYMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSONVTVLRDKLVKCGISLLAQN 139

QY 169 TS 170

DB 140 TS 141

RESULT 7

ABO84755

ID ABO84755 standard; protein; 161 AA.

XX

XX ABO84755;

XX

XX 18-NOV-2004 (first entry)

XX

XX Human cancer-associated protein (CAP) HP07-003.

XX

XX Human; cancer-associated protein; CAP; cancer; cytostatic.

XX

XX Homo sapiens.

XX

XX WO2004058146-A2.

XX

XX 15-JUL-2004.

XX

XX 15-DEC-2003; 2003WO-US040081.

XX

XX 17-DEC-2002; 2002US-00322281.

XX (SAGR-) SAGRES DISCOVERY INC.

XX

XX Morris DW, Malandro MS;

XX WPI; 2004-499109/47.
DR N-PSDB; ABD33081.
XX
PT Novel human cancer associated protein encoded within open reading frame
PT of cancer associated gene, useful as targets for diagnosing cancer.
XX
PS Claim 18; SEQ ID NO 20; 182pp; English.
XX
XX The invention relates to cancer-associated proteins (CAP) and the cancer-
CC associated (CA) nucleic acids encoding them. The invention also relates
CC to a method for treating cancers involving administering to a patient an
CC inhibitor of CAP, and a method of screening for anticancer activity in a
CC potential drug involving providing a cell that expresses a CA gene,
CC contacting a tissue sample derived from a cancer cell with an anticancer
CC drug candidate and monitoring the effect of the anticancer drug candidate
CC on expression of the CA gene. The CAP proteins are useful for detecting
CC cancer associated with expression of a CAP protein in a test cell sample
CC and for screening for a bioactive agent capable of modulating the
CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC cancer, involving determining the expression of a CA nucleic acid in a
CC tissue. This sequence represents a human CAP of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 161 AA;
Query Match 66.7%; Score 630; DB 8; Length 161;
Best Local Similarity 99.2%; Pred. No. 7.9e-54;
Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 49 QKVTSLTACLVDQSLRDLCDREHNTSSSPIQYFSLTRETCKHVLFGTVGVPEHTYRSRTN 108
DB 20 QKVTSLTACLVDQSLRDLCDREHNTSSSPIQYFSLTRETCKHVLFGTVGVPEHTYRSRTN 79
QY 109 FTSKYNMKVLYLSAFTSKDEGTYTTCALHSHGSHSPPISSQNVTVLRDKLVKCEGISLLAQN 168
DB 80 FTSKYNMKVLYLSAFTSKDEGTYTTCALHSHGSHSPPISSQNVTVLRDKLVKCEGISLLAQN 139
QY 169 TS 170
DB 140 TS 141
RESULT 8
AD213572
ID AD213572 standard; protein; 161 AA.
XX
AC AD213572;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human cancer-associated protein #329.
XX
KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
KW cytostatic.
XX
OS Homo sapiens.
XX
FN WO2005031001-A2.
XX
PD 07-APR-2005.
XX
PF 23-SEP-2004; 2004WO-US031617.
XX
PR 23-SEP-2003; 2003US-00669920.
XX
PA (CHIR) CHIRON CORP.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2005-273395/28.

DR N-PSDB; AD213571.
XX
PT Nucleic acid array useful for detecting cancer associated nucleic acid,
PT comprises two or more nucleic acid probes.
XX
PS Disclosure; SEQ ID NO 1092; 198pp; English.
XX
XX The invention relates to a nucleic acid array for detecting a cancer
CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC The invention also relates to a peptide array comprising two or more
CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC that binds to a polypeptide, an isolated antibody or its fragment which
CC binds to a polypeptide, which is prepared by immunizing a host animal
CC with a composition comprising the polypeptide or its antigen binding
CC fragment and collecting cells from the host expressing antibodies against
CC the antigen or its antigen binding fragment, a composition comprising the
CC antibody and a carrier, a method of screening for anticancer activity, a
CC method of detecting a CA nucleic acid, a method of inhibiting expression of a
CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
CC nucleic acids. The antibody is useful for detecting the presence or
CC absence of cancer cells in an individual which involves contacting cells
CC from the individual with the antibody and detecting a complex of a CA
CC protein from the cancer cells and the antibody, where the detection of
CC the complex correlates with the presence of cancer cells in the
CC individual. The composition is useful for inhibiting growth of cancer
CC cells in an individual or for delivering a therapeutic agent to cancer
CC cells in an individual. The invention is also useful for diagnosing
CC cancer, for treating cancer and for inhibiting expression of a CA gene in
CC a cell. This sequence represents a human cancer-associated protein of the
CC invention.
XX
SQ Sequence 161 AA;
Query Match 66.7%; Score 630; DB 9; Length 161;
Best Local Similarity 99.2%; Pred. No. 7.9e-54;
Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 49 QKVTSLTACLVDQSLRDLCDREHNTSSSPIQYFSLTRETCKHVLFGTVGVPEHTYRSRTN 108
DB 20 QKVTSLTACLVDQSLRDLCDREHNTSSSPIQYFSLTRETCKHVLFGTVGVPEHTYRSRTN 79
QY 109 FTSKYNMKVLYLSAFTSKDEGTYTTCALHSHGSHSPPISSQNVTVLRDKLVKCEGISLLAQN 168
DB 80 FTSKYNMKVLYLSAFTSKDEGTYTTCALHSHGSHSPPISSQNVTVLRDKLVKCEGISLLAQN 139
QY 169 TS 170
DB 140 TS 141
RESULT 9
AD213574
ID AD213574 standard; protein; 161 AA.
XX
AC AD213574;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human cancer-associated protein #330.
XX
KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
KW cytostatic.
XX
OS Homo sapiens.
XX
FN WO2005031001-A2.
XX
PD 07-APR-2005.
XX
PF 23-SEP-2004; 2004WO-US031617.
XX
PR 23-SEP-2003; 2003US-00669920.

XX (CHIR) CHIRON CORP.
PA Morris DW, Malandro MS;
PI WPI; 2005-273395/28.
DR N-PSDB; ADZ13573.
XX Nucleic acid array useful for detecting cancer associated nucleic acid,
PT comprises two or more nucleic acid probes.
XX Disclosure; SEQ ID NO 1094; 198pp; English.
XX The invention relates to a nucleic acid array for detecting a cancer
CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC The invention also relates to a peptide array comprising two or more
CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC that binds to a polypeptide, an isolated antibody or its fragment which
CC binds to a polypeptide, which is prepared by immunizing a host animal
CC with a composition comprising the polypeptide or its antigen binding
CC fragment and collecting cells from the host expressing antibodies against
CC the antigen or its antigen binding fragment, a composition comprising the
CC antibody and a carrier, a method of screening for anticancer activity, a
CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a
CC method of treating cancer and a method of inhibiting expression of a CA
CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
CC nucleic acids. The antibody is useful for detecting the presence or
CC absence of cancer cells in an individual which involves contacting cells
CC from the individual with the antibody and detecting a complex of a CA
CC protein from the cancer cells and the antibody, where the detection of
CC the complex correlates with the presence of cancer cells in the
CC individual. The composition is useful for inhibiting growth of cancer
CC cells in an individual or for delivering a therapeutic agent to cancer
CC cells in an individual. The invention is also useful for diagnosing
CC cancer, for treating cancer and for inhibiting expression of a CA gene in
CC a cell. This sequence represents a human cancer-associated protein of the
CC invention.
XX Sequence 161 AA;
SQ
Query Match 66.7%; Score 630; DB 9; Length 161;
Best Local Similarity 99.2%; Pred. No. 7.9e-54;
Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 49 QKVTSLTACLVDQSLRDCRHEHTSSPIQYEFSLTRETKKHVLFCTGVPETHYRSRTN 108
Db 20 QKVTSLTACLVDQSLRDCRHEHTSSPIQYEFSLTRETKKHVLFCTGVPETHYRSRTN 79
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRDKLVKCGISLLAQN 168
Db 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRDKLVKCGISLLAQN 139
QY 169 TS 170
Db 140 TS 141
RESULT 10
ADZ13570
ID ADZ13570 standard; protein; 161 AA.
XX ADZ13570;
AC
XX
DT 16-JUN-2005 (first entry)
XX
XX Human cancer-associated protein #328.
XX Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
KW cytostatic.
KW
XX Homo sapiens.
OS
XX WO2005031001-A2.
PN

XX 07-APR-2005.
XX 23-SEP-2004; 2004WO-US031617.
XX 23-SEP-2003; 2003US-00669920.
XX (CHIR) CHIRON CORP.
XX Morris DW, Malandro MS;
PI WPI; 2005-273395/28.
DR N-PSDB; ADZ13569.
XX Nucleic acid array useful for detecting cancer associated nucleic acid,
PT comprises two or more nucleic acid probes.
XX Disclosure; SEQ ID NO 1090; 198pp; English.
XX The invention relates to a nucleic acid array for detecting a cancer
CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC The invention also relates to a peptide array comprising two or more
CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC that binds to a polypeptide, an isolated antibody or its fragment which
CC binds to a polypeptide, which is prepared by immunizing a host animal
CC with a composition comprising the polypeptide or its antigen binding
CC fragment and collecting cells from the host expressing antibodies against
CC the antigen or its antigen binding fragment, a composition comprising the
CC antibody and a carrier, a method of screening for anticancer activity, a
CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a
CC method of treating cancer and a method of inhibiting expression of a CA
CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
CC nucleic acids. The antibody is useful for detecting the presence or
CC absence of cancer cells in an individual which involves contacting cells
CC from the individual with the antibody and detecting a complex of a CA
CC protein from the cancer cells and the antibody, where the detection of
CC the complex correlates with the presence of cancer cells in the
CC individual. The composition is useful for inhibiting growth of cancer
CC cells in an individual or for delivering a therapeutic agent to cancer
CC cells in an individual. The invention is also useful for diagnosing
CC cancer, for treating cancer and for inhibiting expression of a CA gene in
CC a cell. This sequence represents a human cancer-associated protein of the
CC invention.
XX Sequence 161 AA;
SQ
Query Match 66.7%; Score 630; DB 9; Length 161;
Best Local Similarity 99.2%; Pred. No. 7.9e-54;
Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 49 QKVTSLTACLVDQSLRDCRHEHTSSPIQYEFSLTRETKKHVLFCTGVPETHYRSRTN 108
Db 20 QKVTSLTACLVDQSLRDCRHEHTSSPIQYEFSLTRETKKHVLFCTGVPETHYRSRTN 79
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRDKLVKCGISLLAQN 168
Db 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRDKLVKCGISLLAQN 139
QY 169 TS 170
Db 140 TS 141
RESULT 11
AAB43939
ID AAB43939 standard; protein; 165 AA.
XX AAB43939;
AC
XX
DT 08-FEB-2001 (first entry)
XX
XX Human cancer associated protein sequence SEQ ID NO:1384.
XX

KW Human; cancer associated gene; cancer antigen; detection; cancer;
KW diagnosis; cytostatic; proliferative; vulnerary; immunomodulator;
KW antidiabetic; antiaslathmic; antirheumatic; antiarthritic; antiviral;
KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
KW vasotropic; antiporiatic; antiangiogenic; gene therapy; inflammation;
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW allergic reaction; graft versus host disease; organ rejection;
KW haemostatic; thrombolytic; cardiovascular disorder; infection;
KW neurological disease; drug screening.
XX
OS Homo sapiens.
XX
XX WO200055350-A1.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US005882.
XX
XX 12-MAR-1999; 99US-0124270P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2000-587533/55.
XX
XX N-PSDB; AAC78148.
XX
XX Novel isolated nucleic acids comprising sequences encoding peptides
XX useful for treating or diagnosing e.g. cancer.
XX
XX Claim 11; Page 2053-2054; 2352pp; English.
XX
XX AAC77607 to AAC78448 encode the human cancer associated proteins given in
XX AAB43398 to AAB44239. The proteins can have activities based on the
XX tissues and cells the genes are expressed in. Example of activities
XX include: cytostatic; proliferative; vulnerary; immunomodulator;
XX antidiabetic; antiaslathmic; antirheumatic; antithyroid;
XX antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
XX dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
XX nootropic; vasotropic; antiporiatic and antiangiogenic. The
XX polynucleotides and polypeptides can be used for preventing, treating or
XX ameliorating medical conditions and diagnosing pathological conditions.
XX Polynucleotides, polypeptides, antibodies, agonists and antagonists from
XX the present invention may be used to treat immune disorders by activating
XX or inhibiting the proliferation, differentiation or mobilisation of
XX immune cells, to treat disorders of haematopoietic cells, autoimmune
XX disorders, allergic reactions, graft versus host disease and organ
XX rejection, modulate haemostatic or thrombolytic activity, modulate
XX inflammation, cancers, cardiovascular disorders, neurological disease and
XX bacterial or viral infections. The peptides, nucleotides, antibodies,
XX agonists and antagonists may be also be used in drug screens. AAC78449 to
XX AAC78457 and AAB44240 represent sequences used in the exemplification of
XX the present invention
XX
SQ Sequence 165 AA;

Query Match 66.7%; Score 630; DB 3; Length 165;
Best Local Similarity 99.2%; Pred. No. 8.2e-54;
Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 49 QKVTSLTACLVDOSLRDCHRENTSSPIQYFSLTRTKKHLVFGTVGVPEHTYRSRTN 108
DB 24 QKVTSLTACLVDOSLRDCHRENTSSPIQYFSLTRTKKHLVFGTVGVPEHTYRSRTN 83
QY 109 FTSKYRMKVLVLSAFTSKDEGTYTTCALHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 168
DB 84 FTSKYRMKVLVLSAFTSKDEGTYTTCALHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 143
QY 169 TS 170
DB 144 TS 145

RESULT 12
AAG73850
ID AAG73850 standard; protein; 165 AA.
XX
AC AAG73850;
XX
DT 03-SEP-2001 (first entry)
XX
XX Human colon cancer antigen protein SEQ ID NO:4614.
XX
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome 11.
XX
XX Homo sapiens.
XX
XX WO200122920-A2.
XX
XX 05-APR-2001.
XX
XX 28-SEP-2000; 2000WO-US026524.
XX
XX 29-SEP-1999; 99US-0157137P.
PR 03-NOV-1999; 99US-0163280P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Barash SC, Birse CE, Rosen CA;
PI
XX WPI; 2001-235357/24.
XX
XX N-PSDB; AAB33281.
XX
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers.
XX
XX Claim 11; Page 6411-6412; 9803pp; English.
XX
XX AAB32943 to AAB37195 and AAG73514 to AAG77788 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where the
XX proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytostatic activity and can be used in gene therapy
XX and vaccine production. N and P may be used in the prevention, diagnosis
XX and treatment of diseases associated with inappropriate P expression. For
XX example, N and P may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of P by expressing inactive proteins or to
XX supplement the patients own production of P. Additionally, N may be used
XX to produce the colon cancer-associated Ps, by inserting the nucleic acids
XX into a host cell and culturing the cell to express the proteins. N and P
XX can be used in the prevention, diagnosis and treatment of colorectal
XX carcinomas and cancers. AAB37196 to AAB37204 and AAB77789 represent
XX sequences used in the exemplification of the present invention. N.B.
XX Pages 666 to 682 and page 7053 of the sequence listing were missing at
XX time of publication, meaning no sequences are present for SEQ ID NO:1027
XX to 1052, 7921 and 7922
XX
SQ Sequence 165 AA;

Query Match 66.7%; Score 630; DB 4; Length 165;
Best Local Similarity 99.2%; Pred. No. 8.2e-54;
Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 49 QKVTSLTACLVDOSLRDCHRENTSSPIQYFSLTRTKKHLVFGTVGVPEHTYRSRTN 108
DB 24 QKVTSLTACLVDOSLRDCHRENTSSPIQYFSLTRTKKHLVFGTVGVPEHTYRSRTN 83
QY 109 FTSKYRMKVLVLSAFTSKDEGTYTTCALHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 168
DB 84 FTSKYRMKVLVLSAFTSKDEGTYTTCALHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 143
QY 169 TS 170
DB 144 TS 145

```
RESULT 13
ADW10183
ID ADW10183 standard; protein; 162 AA.
XX
XX ADW10183;
XX
XX
DT 24-MAR-2005 (first entry)
XX
XX Human Thy-1 protein.
XX
XX non-immunoglobulin binding polypeptide; selective binding; Thy-1.
XX
XX Homo sapiens.
XX
XX US2004266993-A1.
XX
XX 30-DEC-2004.
XX
XX 30-JUN-2003; 2003US-00611655.
XX
XX 30-JUN-2003; 2003US-00611655.
XX
XX (EVAN/) EVANS G A.
XX
XX Evans GA;
XX
XX WPI; 2005-047648/05.
XX
XX New chimeric non-immunoglobulin binding polypeptide comprises
PT immunoglobulin-like domain containing scaffold and exhibits selective
PT binding activity; for producing non-immunoglobulin binding polypeptides
PT with selective binding activity.
XX
XX Disclosure; SEQ ID NO 1; 45pp; English.
XX
XX The invention relates to a novel chimeric non-immunoglobulin binding
CC polypeptide. The polypeptide comprises an immunoglobulin-like domain
CC containing scaffold with two or more solvent exposed loops containing a
CC different complementarity-determining region (CDR) from a parent antibody
CC inserted into each of the loops and exhibiting selective binding activity
CC toward a ligand bound by the parent antibody. The invention further
CC comprises a chimeric ThyOx binding polypeptide, comprising one or more
CC altered immunoglobulin-like domain loop regions of a ThyOx family
CC polypeptide or at least one immunoglobulin-like domain containing
CC scaffold derived from a ThyOx family polypeptide, and a heterologous
CC binding polypeptide exhibiting selective binding activity toward a non-
CC ThyOx ligand; and a nucleic acid encoding the non-immunoglobulin or ThyOx
CC binding polypeptide above. The chimeric non-immunoglobulin binding
CC polypeptide is useful for producing non-immunoglobulin binding
CC polypeptides having selective binding activity toward a predetermined
CC molecule. This sequence represents a human Thy-1 protein of the
CC invention.
XX
XX Sequence 162 AA;
SQ
Query Match 65.4%; Score 617.5; DB 9; Length 162;
Best Local Similarity 98.4%; Pred. No. 1.4e-52;
Matches 121; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 49 QKVTSLTACLVDQSLRDLCHRENTSSSPIQYEFSLTRETCKGVLFGTVGPVPHYRSRTN 108
Db 20 QKVTSLTACLVDQSLRDLCHRENTSSSPIQYEFSLTRETCKGVLFGTVGPVPHYRSRTN 79
QY 109 FTSKYMVKVLYLSAFTSKDEGTYTTCALHSHSGHSPPI-SSQNTVTLRDKLKVCBGISLLAQ 167
Db 80 FTSKYMVKVLYLSAFTSKDEGTYTTCALHSHSGHSPPISSQNTVTLRDKLKVCBGISLLAQ 139
QY 168 NTS 170
Db 140 NTS 142
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RESULT 14
AAY31789
ID AAY31789 standard; protein; 368 AA.
XX
XX AAY31789;
XX
XX 17-OCT-2003 (revised)
DT 06-DEC-1999 (first entry)
XX
XX Human Thy-1-human IgG constant region fusion protein.
XX
XX Thy-1; human; IgG; angiogenesis; cancer; tumour; rheumatoid arthritis;
XX atherosclerosis; therapy.
XX
XX Homo sapiens.
XX
XX Chimeric.
XX
XX Key Location/Qualifiers
FT Peptide 1..19
FT /note= "Thy-1 signal peptide"
FT Protein 18..368
FT /note= "Thy-1-Ig fusion, specifically claimed in Claim 8"
XX
XX WO9945951-A2.
XX
XX 16-SEP-1999.
XX
XX 11-MAR-1999; 99WO-US005256.
XX
XX 11-MAR-1998; 98US-00077524.
XX
XX (HARD ) HARVARD COLLEGE.
XX (HABE/) HABER C.
XX
XX Haber E, Shaw S, Jain MK, Lee W;
XX
XX WPI; 1999-561618/47.
XX N-PSDB; AAX87980.
XX
XX Inhibiting Thy-1 expression in endothelial cell, useful for inhibiting
PT angiogenesis.
XX
XX Claim 8; Page 46-47; 47pp; English.
XX
XX The present sequence represents a fusion protein, the mature region of
CC which is claimed, comprising the human Thy-1 extracellular region (see
CC AAY31787) and the constant region (hinge, CH2, CH3) of human IgG1. A
CC claimed method for inhibiting angiogenesis in a mammal comprises
CC administering a compound that inhibits Thy-1 associated proliferation of
CC an endothelial cell. The compound is preferably the extracellular region
CC of rat or human Thy-1. The method is used in the treatment of a mammal
CC having a tumour (e.g. by reducing vascularisation), atherosclerosis or
CC rheumatoid arthritis, the lesions of which may be associated with
CC neovascularisation (all claimed). Another claimed method for inhibiting
CC angiogenesis involves administering a Thy-1 antisense nucleic acid or a
CC Thy-1-specific antibody linked to a cytotoxic agent. A method for
CC promoting angiogenesis involves administering a compound that increases
CC Thy-1 expression in an endothelial cell such as a chimeric protein
CC comprising the Thy-1 extracellular fragment and the constant region of an
CC immunoglobulin. (Updated on 17-OCT-2003 to standardise OS field)
XX
XX Sequence 368 AA;
SQ
Query Match 64.0%; Score 604; DB 2; Length 368;
Best Local Similarity 91.3%; Pred. No. 8.2e-51;
Matches 116; Conservative 2; Mismatches 9; Indels 0; Gaps 0;
QY 49 QKVTSLTACLVDQSLRDLCHRENTSSSPIQYEFSLTRETCKGVLFGTVGPVPHYRSRTN 108
Db 20 QKVTSLTACLVDQSLRDLCHRENTSSSPIQYEFSLTRETCKGVLFGTVGPVPHYRSRTN 79
QY 109 FTSKYMVKVLYLSAFTSKDEGTYTTCALHSHSGHSPPISSQNTVTLRDKLKVCBGISLLAQ 168
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Db 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDKLVKCEGADLSRP 139
QY 169 TSHHHH 175
Db 140 KSSDKTH 146

Search completed: December 6, 2005, 10:36:50
Job time : 165.348 secs

RESULT 15
AAY31787
ID AAY31787 standard; protein; 119 AA.
XX AC AAY31787;
XX DT 06-DEC-1999 (first entry)
XX DE Human Thy-1 extracellular fragment.
XX KW Thy-1; human; angiogenesis; cancer; tumour; rheumatoid arthritis;
XX KW atherosclerosis; therapy.
XX OS Homo sapiens.
XX PN WO9945951-A2.
XX PD 16-SEP-1999.
XX PF 11-MAR-1999; 99WO-US005256.
XX PR 11-MAR-1998; 98US-00077524.
XX PA (HARD) HARVARD COLLEGE.
XX PA (HABE/) HABER C.
XX PI Haber E, Shaw S, Jain MK, Lee W;
XX WPI; 1999-561618/47.
XX Inhibiting Thy-1 expression in endothelial cell, useful for inhibiting
XX angiogenesis.
XX Claim 6; Page 4; 47pp; English.
XX The present sequence represents the extracellular region of human Thy-1,
XX a protein expressed by vascular endothelial cells during angiogenesis. A
XX claimed method for inhibiting angiogenesis in a mammal comprises
XX administering a compound that inhibits Thy-1 associated proliferation of
XX an endothelial cell. This compound is preferably the extracellular region
XX of human or rat (see AAY31786) Thy-1. The method is used in the treatment
XX of a mammal having a tumour (e.g. by reducing vascularisation),
XX atherosclerosis and rheumatoid arthritis, the lesions of which may be
XX associated with neovascularisation (all claimed). Another claimed method
XX for inhibiting angiogenesis involves administering a Thy-1 antisense
XX nucleic acid or a Thy-1-specific antibody linked to a cytotoxic agent. A
XX method for promoting angiogenesis involves administering a compound that
XX increases Thy-1 expression in an endothelial cell such as a chimeric
XX protein comprising the Thy-1 extracellular fragment and the constant
XX region of an immunoglobulin (see AAY31788)
XX SQ Sequence 119 AA;
Query Match 63.6%; Score 600; DB 2; Length 119;
Best Local Similarity 98.3%; Pred. No. 4.9e-51;
Matches 114; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 49 QKVTSLTACLVDSQSLRDCHEHTSSPIQYEFSLTRETCKHVLFGTVGVPEHTYRSRTN 108
Db 1 QKVTSLTACLVDSQSLRDCHEHTSSPIQYEFSLTRETCKHVLFGTVGVPEHTYRSRTN 60
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDKLVKCEGADLS 164
Db 61 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDKLVKCEGADLS 116

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OM protein - protein search, using sw model

Run on: December 6, 2005, 10:37:02 ; Search time 4.64111 Seconds
(without alignments)
114.521 Million cell updates/sec

Title: US-10-611-655-4

Perfect score: 605

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

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- 3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
- 5: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	118	19.5	121	7	US-11-108-135-28
2	115	19.0	122	6	US-10-932-334-73
3	109	18.0	120	6	US-10-932-334-71
4	109	18.0	120	6	US-10-932-334-72
5	101	16.7	248	6	US-10-512-184-36
6	101	16.7	615	6	US-10-512-184-50
7	100	16.5	121	7	US-11-108-135-24
8	100	16.5	123	6	US-10-932-334-87
9	100	16.5	123	6	US-10-932-334-88
10	100	16.5	123	6	US-10-932-334-92
11	100	16.5	124	6	US-10-932-334-7
12	100	16.5	124	6	US-10-932-334-13
13	100	16.5	124	6	US-10-932-334-70
14	100	16.5	143	6	US-10-932-334-52
15	99	16.4	98	6	US-10-932-334-57
16	97.5	16.1	248	7	US-11-054-515-2088
17	97	16.0	247	7	US-11-054-515-2103
18	96	15.9	120	6	US-10-932-334-74
19	92	15.2	120	7	US-11-173-071-2
20	92	15.2	121	6	US-10-507-662-25
21	92	15.2	121	6	US-10-507-662-26
22	90	14.9	138	7	US-11-089-872-3
23	87	14.4	255	7	US-11-054-515-2087
24	87	14.4	257	7	US-11-054-515-1514
25	86	14.2	115	6	US-10-932-334-80

Sequence 21, Appl
Sequence 1919, Ap
Sequence 2084, Ap
Sequence 1995, Ap
Sequence 32, Appl
Sequence 57, Appl
Sequence 21, Appl
Sequence 47, Appl
Sequence 50, Appl
Sequence 35, Appl
Sequence 77, Appl
Sequence 79, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 29, Appl
Sequence 1418, Ap
Sequence 1672, Ap
Sequence 30, Appl

26 14.2 86 121 6 US-10-502-145-21
27 86 14.2 245 7 US-11-054-515-1919
28 85 14.0 242 7 US-11-054-515-2084
29 84.5 14.0 248 7 US-11-054-515-1995
30 84 13.9 118 6 US-10-507-662-32
31 84 13.9 125 7 US-11-096-074-57
32 83.5 13.8 247 7 US-11-084-717-21
33 83 13.7 118 6 US-10-932-334-75
34 82.5 13.6 116 7 US-11-065-943-47
35 82 13.6 114 7 US-11-096-074-50
36 82 13.6 118 6 US-10-507-662-35
37 82 13.6 120 6 US-10-932-334-77
38 82 13.6 120 6 US-10-932-334-79
39 82 13.6 121 6 US-10-932-334-81
40 82 13.6 128 7 US-11-173-071-12
41 82 13.6 128 7 US-11-173-071-14
42 82 13.6 136 6 US-10-839-799-29
43 82 13.6 253 7 US-11-054-515-1418
44 82 13.6 253 7 US-11-054-515-1672
45 81 13.4 118 6 US-10-507-662-30

ALIGNMENTS

RESULT 1
US-11-108-135-28
; Sequence 28, Application US/11108135
; Publication No. US20050260213A1
; GENERAL INFORMATION:
; APPLICANT: Koenig, Scott
; APPLICANT: Veri, Maria Concetta
; APPLICANT: Tuailon, Nadine
; APPLICANT: Bonvinl, Ezio
; APPLICANT: Stavenhagen, Jeffrey
; APPLICANT: Rankin, Christopher
; TITLE OF INVENTION: FC-gamma-RIIB-specific antibodies and methods of use thereof
; FILE REFERENCE: 11183-014-999
; CURRENT APPLICATION NUMBER: US/11/108,135
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/562,804
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/582,044
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/582,045
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/654,713
; PRIOR FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 121
; TYPE: PRT
; ORGANISM: mus sp.
; FEATURE:
; OTHER INFORMATION: Mouse 2B6 heavy chain variable region
US-11-108-135-28

Query Match 19.5%; Score 118; DB 7; Length 121;
Best Local Similarity 33.3%; Pred. No. 9.2e-07;
Matches 29; Conservative 14; Mismatches 42; Indels 2; Gaps 1;
QY 1 QVSRGQKVTSLTACLVQDQLRDCRHNTSSNNYWHFSLTRTKKHLVFGTTDPADSYT 60
Db 1 QVQLQCPVTELVLR--PGASVMTLSCKASDYPFTNYIHWVKRPGQGLEWIGVIDPSDTP 58
QY 61 SYNQNKFGSGTYTCALHSHGSHPPISS 87
Db 59 NYNKKFKGKATLTVVVVSSSTAYNQQLSS 85
RESULT 2
US-10-932-334-73

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; Sequence 73, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-73

Query Match          19.0%; Score 115; DB 6; Length 122;
Best Local Similarity 28.7%; Pred. No. 2e-06;
Matches 25; Conservative 19; Mismatches 41; Indels 2; Gaps 1;

QY 19 SRLDCRHEHTSSSNMWFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGTYTCALHH 78
   |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 17 SVKLSCKASGYFTFTSYMMHWKQPGQGLEWIGRIDPSDYPNFKGKATLT--VDK 74
   |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
QY 79 SGHSPPISSQNTVLRDLKLVKCEGVY 105
   |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 75 SSTAYMQLSSLTSEDSAVYCYCASLY 101
   |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

RESULT 3
US-10-932-334-71
; Sequence 71, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 71
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-71

Query Match          18.0%; Score 109; DB 6; Length 120;
Best Local Similarity 31.7%; Pred. No. 8.9e-06;
Matches 32; Conservative 11; Mismatches 42; Indels 16; Gaps 4;

QY 19 SRLDCRHEHTSSSNMWFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGTYTCALHH 78
   |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 17 SVKLSCKASGYFTFTSYMMHWKQPGQGLEWIGRIDPSDYPNFKGKATLT--VDK 74
   |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
QY 79 SGHSPPISSQNTVLRDLKLVKCEGVY--RY-----YFDY 111
   |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 73 ---DKP-SSTAYMQLSSLTSEDSAVYCYARYDYGGSSYFDY 109
   |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

RESULT 4
US-10-932-334-72
; Sequence 72, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-72

Query Match          18.0%; Score 109; DB 6; Length 120;
Best Local Similarity 31.7%; Pred. No. 8.9e-06;
Matches 32; Conservative 11; Mismatches 42; Indels 16; Gaps 4;

QY 19 SRLDCRHEHTSSSNMWFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGTYTCALHH 78
   |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 17 SVKLSCKASGYFTFTSYMMHWKQPGQGLEWIGRIDPSDYPNFKGKATLT--VDK 72
   |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
QY 79 SGHSPPISSQNTVLRDLKLVKCEGVY--RY-----YFDY 111
   |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 79 STAYMELSS--LTNEDSAVYICTRTDWDYAMDY 109
   |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
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Query Match      16.5%; Score 100; DB 6; Length 123;
Best Local Similarity 26.0%; Pred. No. 9e-05;
Matches 27; Conservative 17; Mismatches 40; Indels 20; Gaps 2;

Qy 19 SLRLDCHRENTSSNYMHFSLTRETKKHVLFGTIDPADSYTSYNQNFDEGTVTCALHH 78
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
pb 17 SVKI
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Search completed: December 6, 2005, 10:48:05
Job time : 5.64111 secs

Db 17 SVKLSCKASGYTFTSYMMHWKQRPQGLEWIGINPNSGRITNNYNEKFKRKATLTV----- 72

Qy 79 SGHSPPISSQNTVLRDLKVKCEGVY-----RYFFD 110

Db 73 ----DKSSSTAYMQLSSLTSDSAVYYPARGRPDYGGSSKWYFD 112

RESULT 14

US-10-932-334-52
; Sequence 52, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-1 RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-932-334-52

Query Match 16.5%; Score 100; DB 6; Length 143;
Best Local Similarity 26.0%; Pred. No. 0.00011;
Matches 27; Conservative 17; Mismatches 40; Indels 20; Gaps 2;

Qy 19 SLRLDCRHEHTSSNWMHFSLTRETKKHVLFGTIDPADSYTSYNQNFKEGTYTCALHH 78

Db 36 SVKLSCKASGYTFTSYMMHWKQRPQGLEWIGINPNSGRITNNYNEKFKRKATLTV----- 91

Qy 79 SGHSPPISSQNTVLRDLKVKCEGVY-----RYFFD 110

Db 92 ----DKSSSTAYMQLSSLTSDSAVYYPARGRPDYGGSSKWYFD 131

RESULT 15

US-10-932-334-57
; Sequence 57, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-932-334-57

Query Match 16.4%; Score 99; DB 6; Length 98;
Best Local Similarity 32.7%; Pred. No. 8.9e-05;
Matches 18; Conservative 14; Mismatches 23; Indels 0; Gaps 0;

Qy 19 SLRLDCRHEHTSSNWMHFSLTRETKKHVLFGTIDPADSYTSYNQNFKEGTYT 73

Db 17 SVKLSCKASGYTFTSYMMHWKQRPQGLEWIGINPNSGRITNNYNEKFKSKATLT 71

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: December 6, 2005, 10:32:13 ; Search time 25.9129 Seconds
(without alignments)
354.148 Million cell updates/sec

Title: US-10-611-655-4
Perfect score: 605
Sequence: 1 QVSRGQKVTSLTACLVDSQSL.....VLRDLKLVKCEGVYRYFDY 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/aaa/6 COMB.pep.*
3: /cgn2_6/prodata/1/aaa/H COMB.pep.*
4: /cgn2_6/prodata/1/aaa/PCTUS COMB.pep.*
5: /cgn2_6/prodata/1/aaa/RE COMB.pep.*
6: /cgn2_6/prodata/1/aaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	424	70.1	161	2 US-09-949-016-11168	Sequence 11168, A
2	242.5	40.1	105	2 US-09-513-999C-4247	Sequence 4247, App
3	126	20.8	120	2 US-10-092-246-12	Sequence 12, Appl
4	126	20.8	120	2 US-10-096-246A-12	Sequence 12, Appl
5	125.5	20.7	119	1 US-08-553-497A-12	Sequence 12, Appl
6	125	20.7	117	2 US-09-065-059-15	Sequence 15, Appl
7	125	20.7	117	2 US-08-913-555-15	Sequence 15, Appl
8	124.5	20.6	116	1 US-08-672-345C-17	Sequence 17, Appl
9	124.5	20.6	116	2 US-09-214-095D-17	Sequence 17, Appl
10	124.5	20.6	116	2 US-09-940-727B-17	Sequence 17, Appl
11	123.5	20.4	119	2 US-08-767-128-6	Sequence 6, Appl
12	123	20.3	113	1 US-08-273-146-59	Sequence 59, Appl
13	123	20.3	113	2 US-09-214-095D-118	Sequence 118, App
14	123	20.3	113	2 US-09-940-727B-118	Sequence 118, App
15	122.5	20.2	111	2 US-08-881-037-14	Sequence 14, Appl
16	122.5	20.2	119	2 US-08-881-037-62	Sequence 62, Appl
17	122.5	20.2	146	2 US-09-069-628-30	Sequence 30, Appl
18	121.5	20.1	119	1 US-08-553-497A-8	Sequence 8, Appl
19	121.5	20.1	119	1 US-08-800-198-2	Sequence 2, Appl
20	121.5	20.1	119	2 US-09-296-595-2	Sequence 2, Appl
21	121.5	20.1	240	1 US-08-800-198-8	Sequence 8, Appl
22	121.5	20.1	240	2 US-09-595-595-8	Sequence 8, Appl
23	121	20.0	98	2 US-08-881-037-59	Sequence 59, Appl
24	120.5	19.9	111	2 US-08-881-037-17	Sequence 17, Appl
25	120.5	19.9	119	2 US-08-881-037-63	Sequence 63, Appl
26	119.5	19.8	111	2 US-08-881-037-16	Sequence 16, Appl
27	119.5	19.8	119	2 US-08-881-037-61	Sequence 61, Appl

28 118 19.5 119 2 US-09-406-532-2 Sequence 2, Appli
29 116 19.2 114 2 US-09-726-219A-226 Sequence 226, App
30 116 19.2 114 2 US-09-196-522-226 Sequence 226, App
31 116 19.2 118 2 US-09-698-705-9 Sequence 9, Appli
32 115.5 19.1 111 2 US-08-881-037-15 Sequence 15, Appl
33 115.5 19.1 119 2 US-08-881-037-60 Sequence 60, Appl
34 114 18.8 116 1 US-08-690-102A-4 Sequence 4, Appli
35 114 18.8 116 2 US-09-121-902-4 Sequence 4, Appli
36 114 18.8 116 2 US-09-155-107-4 Sequence 4, Appli
37 114 18.8 116 4 PCT-US95-09641-4 Sequence 4, Appli
38 113 18.7 256 2 US-09-526-738A-2 Sequence 2, Appli
39 113 18.7 258 1 US-08-621-751A-12 Sequence 12, Appl
40 112 18.5 135 1 US-08-621-751A-12 Sequence 12, Appl
41 112 18.5 142 2 US-09-069-628-27 Sequence 27, Appl
42 112 18.5 241 1 US-08-235-838-11 Sequence 11, Appl
43 112 18.5 241 1 US-08-465-473B-11 Sequence 11, Appl
44 112 18.5 637 1 US-08-235-838-16 Sequence 16, Appl
45 112 18.5 637 1 US-08-465-473B-16 Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-11168
; Sequence 11168, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11168
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11168

Query Match 70.1%; Score 424; DB 2; Length 161;
Best Local Similarity 73.9%; Pred. No. 1.1e-40;
Matches 88; Conservative 3; Mismatches 12; Indels 16; Gaps 3;
Qy 1 QVSRGQKVTSLTACLVDSQSLRDLCKHENTSSSNYNWHPSLTRETKKHVLFGTID-PADSY 59
Db 15 QVSRGQKVTSLTACLVDSQSLRDLCKHENTSSSIQYEFSLTRETKKHVLFGTGVVEHY 74
Qy 60 TS-----YNNQNF-----KDEGTYTCALHSHGSPPISSQNTVLRDLKLVKCEGV 103
Db 75 RRTNFTSKYNNKVLVLSAFTSKDEGTYTCALHSHGSPPISSQNTVLRDLKLVKCEGI 133

RESULT 2
US-09-513-999C-4247
; Sequence 4247, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C

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; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1993-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4247
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -19...-1
; OTHER INFORMATION: score 11.7
; OTHER INFORMATION: seq IALLTLVLQVSRG/QK
US-09-513-999C-4247

Query Match          40.1%; Score 242.5; DB 2; Length 105;
Best Local Similarity 62.5%; Pred. No. 3.6e-20;
Matches 55; Conservative 6; Mismatches 16; Indels 11; Gaps 3;

QY 1 QVSRGQKVTSLTACLVDSLRLDCHRENTSSNNYMHFSLTRETKKHVLFGTID-PADSY 59
Db 15 QVSRGQKVTSLTACLVDSLRLDCHRENTSSSPIQVFEFSLTRETKKHVLFGTVGPETHY 74
QY 60 ---TSYNQNFKDEGT-----TCALH 77
Db 75 RRTNFTSKYNNKMKVLYLSASLARTRALH 102

RESULT 3
US-10-092-246-12
; Sequence 12, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of M
; TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/092,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-12

Query Match          20.8%; Score 126; DB 2; Length 120;
Best Local Similarity 32.6%; Pred. No. 9.4e-07;
Matches 31; Conservative 16; Mismatches 44; Indels 4; Gaps 2;

QY 19 SRLDCRHEHTSSNNYMHFSLTRETKKHVLFGTIDPADSYTSYNQNFKDEGTTCALHH 78
Db 17 SVKLSCKASGYFTTSYMHVWKQRPQGGLWGEIDPSDSYTYNQKFKGKATLT--VDK 74
QY 79 SGHSPPISSQNTVLRDLKLVKCEGVY--RYFFDY 111
Db 75 SSSTAYMQPSSLTSEDSAVYICARRYGSRVSMY 109

RESULT 4
US-10-096-246A-12
; Sequence 12, Application US/10096246A
; Patent No. 6818748
; GENERAL INFORMATION:
; APPLICANT: Fulton, R. Elaine
; APPLICANT: Nagata, Leslie
; APPLICANT: Alvi, Azhar Z.
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of
```

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; TITLE OF INVENTION: Monoclonal ScFv Antibody Against Venezuelan Equine Encephalitis
; TITLE OF INVENTION: Virus (VEE)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/096,246A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 12
; LENGTH: 120
; TYPE: PRT
; ORGANISM: mouse
US-10-096-246A-12

Query Match          20.8%; Score 126; DB 2; Length 120;
Best Local Similarity 32.6%; Pred. No. 9.4e-07;
Matches 31; Conservative 16; Mismatches 44; Indels 4; Gaps 2;

QY 19 SRLDCRHEHTSSNNYMHFSLTRETKKHVLFGTIDPADSYTSYNQNFKDEGTTCALHH 78
Db 17 SVKLSCKASGYFTTSYMHVWKQRPQGGLWGEIDPSDSYTYNQKFKGKATLT--VDK 74
QY 79 SGHSPPISSQNTVLRDLKLVKCEGVY--RYFFDY 111
Db 75 SSSTAYMQPSSLTSEDSAVYICARRYGSRVSMY 109

RESULT 5
US-08-553-497A-12
; Sequence 12, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTLEBOROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSSOW, DETLEF
; APPLICANT: ADAN, JAUME
; APPLICANT: MITJANS, FRANCESC
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCESC
; APPLICANT: PIULATS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,497A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/00978
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94104160.0
; FILING DATE: 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94118970.6
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1726
; TELECOMMUNICATION INFORMATION:
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19 SLRLDCRHEHTSSSNYWMHFSLTRETQKHVLFGTIDPADSYTSYNQNFKDEGTYTCALHH 78


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; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-767-128-6

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Query Match 20.4%; Score 123.5; DB 2; Length 119;
Best Local Similarity 32.3%; Pred. No. 1.8e-06;
Matches 30; Conservative 17; Mismatches 43; Indels 3; Gaps 2;

QY 20 LRLDCRHEHTSSNNYMHFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGTYTCALHHS 79
Db 18 VKLSCKASGYTFTSYMMHWKQRPQGLEWIGRIDPSQSETHYNQKFKDKATLT--VDKS 75

QY 80 GHSPPISQNVTVLRDKLVKCGVYRY--FDY 111
Db 76 SSTAYQLSSLT--SSESAVYCARHHYGYAMDY 108

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RESULT 12
US-08-273-146-59
; Sequence 59, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kanten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Titmas, Richard C.
; APPLICANT: Williams, Richard O.
; TITLE OF INVENTION: The Isolation and Production of
; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IGEN, Inc.
; STREET: 1530 East Jefferson St.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20852
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/273,146
; FILING DATE: 14-JUL-1994

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ryan, John W.
; REGISTRATION NUMBER: 33,771
; REFERENCE/DOCKET NUMBER: 09000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-984-8000
; TELEFAX: 301-230-0158
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-273-146-59

Query Match 20.3%; Score 123; DB 1; Length 113;
Best Local Similarity 31.2%; Pred. No. 1.9e-06;
Matches 29; Conservative 15; Mismatches 47; Indels 2; Gaps 1;

QY 19 SLRLDCRHEHTSSNNYMHFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGTYTCALHH 78
Db 17 SVKMSCKASGYTFTSYMMHWKQRPQGLEWIGYINPSTGYTYNQKFKDKATLTADKSS 76

QY 79 SGHSPPISQNVTVLRDKLVKCGVYRY--FDY 111
Db 77 STAYMQLSS--LTSESAVYCARHLYYAMDY 107

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RESULT 13
US-09-214-095D-118
; Sequence 118, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 118
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murine
US-09-214-095D-118

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Query Match 20.3%; Score 123; DB 2; Length 113;
Best Local Similarity 32.6%; Pred. No. 1.9e-06;
Matches 31; Conservative 18; Mismatches 36; Indels 10; Gaps 3;

QY 19 SLRLDCRHEHTSSNNYMHFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGTYTCALHH 78
Db 16 SVKMSCKASGYTFTSYMMHWKQRPQGLEWIGTIDLSYTYGYNQNFKGRATLT--LDE 73

QY 79 SGHSPPISQNVTVLRDKLVKCGVY--RYTFDY 111
Db 74 SENTAYMQLSSLT-----SEDSAVYCSRRGFY 102

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RESULT 14
US-09-940-727B-118
; Sequence 118, Application US/09940727B
; Patent No. 6913917
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 6, 2005, 10:32:12 ; Search time 114.094 Seconds
(without alignments)
686.395 Million cell updates/sec

Title: US-10-611-655-4
Perfect score: 605
Sequence: 1 QVSRGQKVTSLACLVDQSL.....VLRDKLVKCEGVYRYFYDF 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_spot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	424	70.1	161	1	THY1 HUMAN
2	418	69.1	161	1	Q5R508 PONPY
3	417	68.9	161	1	THY1 MACMU
4	377	62.3	145	2	Q59G80 HUMAN
5	332	54.9	161	2	Q9WRU5 CAVPO
6	291.5	48.2	162	1	THY1 MOUSE
7	291.5	48.2	162	2	Q53YX2 MOUSE
8	280	46.3	161	1	THY1 RAT
9	189	31.2	160	2	Q7T252 CHICK
10	176.5	29.2	160	1	THY1 CHICK
11	132	21.8	143	2	Q924P9 MOUSE
12	130	21.5	143	2	Q91V67 MOUSE
13	126	20.8	114	2	Q9JL81 MOUSE
14	118.5	19.6	146	2	Q924R8 MOUSE
15	117	19.3	616	2	Q504M7 MOUSE
16	114.5	18.9	142	2	Q924Q2 MOUSE
17	113	18.7	617	2	Q4KML5 MOUSE
18	111.5	18.4	481	2	Q91WT3 MOUSE
19	109	18.0	139	1	HV07 MOUSE
20	109	18.0	145	2	Q924Q7 MOUSE
21	107.5	17.8	140	2	Q924P8 MOUSE
22	105.5	17.4	570	2	Q5B3J1 BRAKE
23	105	17.4	143	2	Q924Q5 MOUSE
24	104	17.2	117	1	HV06 MOUSE
25	103	17.0	117	1	HV05 MOUSE
26	103	17.0	488	2	Q8K0F2 MOUSE
27	102.5	16.9	470	2	Q7TWK1 MOUSE
28	102	16.9	137	2	Q924R6 MOUSE
29	102	16.9	145	2	Q924R3 MOUSE
30	102	16.9	146	2	Q924Q3 MOUSE
31	101	16.7	60	2	Q9XT67 CANFA

32	101	16.7	119	2	Q9GYZ2 MOUSE	Q9GYZ2 mus musculus
33	101	16.7	120	1	HV50 MOUSE	P06329 mus musculus
34	101	16.7	145	2	Q924R4 MOUSE	Q924R4 mus musculus
35	100.5	16.6	144	2	Q924P5 MOUSE	Q924P5 mus musculus
36	100	16.5	117	1	HV49 MOUSE	P06328 mus musculus
37	99.5	16.4	140	2	Q924E2 MOUSE	Q924E2 mus musculus
38	99	16.4	117	1	HV09 MOUSE	P01753 mus musculus
39	99	16.4	141	2	Q924Q4 MOUSE	Q924Q4 mus musculus
40	99	16.4	142	2	Q924Q1 MOUSE	Q924Q1 mus musculus
41	99	16.4	143	2	Q91VA2 MOUSE	Q91VA2 mus musculus
42	99	16.4	143	2	Q924R7 MOUSE	Q924R7 mus musculus
43	99	16.4	143	2	Q924R0 MOUSE	Q924R0 mus musculus
44	99	16.4	145	2	Q924P7 MOUSE	Q924P7 mus musculus
45	99	16.4	145	2	Q924Q6 MOUSE	Q924Q6 mus musculus

ALIGNMENTS

RESULT 1
ID THY1 HUMAN STANDARD; PRT; 161 AA.
AC P04216; Q16008; Q9NSP1;
DT 20-MAR-1987 (Rel. 04, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE ThY-1 membrane glycoprotein precursor (Thy-1 antigen) (CD90) (CD90 antigen).
DE antigein).
GN Name=THY1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86016759; PubMed=2864690;
RA Seki T., Spurr N., Obata F., Goyert S., Goodfellow P., Silver J., RT "The human Thy-1 gene: structure and chromosomal location.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:6657-6661(1985).
RN [2].
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20403900; PubMed=10944468; DOI=10.1006/bbrc.2000.3282;
RA Ye Z., Connor J.R.;
RT "cDNA cloning by amplification of circularized first strand cDNAs reveals non-IRF-regulated iron-responsive mRNAs.";
RL Biochem. Biophys. Res. Commun. 275:223-227(2000).
RN [3].
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Amysgdala;
RG The German cDNA consortium;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RA [4].
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain, and Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K., Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Guarnatone P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

```
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [5]
RX NUCLEOTIDE SEQUENCE OF 1-55.
RA MEDLINE:93240114; PubMed:7683034; DOI=10.1094/jem.177.5.1331;
RA Craig W., Kay R., Cutler R.L., Landsorp P.M.;
RT "Expression of Thy-1 on human hematopoietic progenitor cells.";
RL J. Exp. Med. 177:1331-1342(1993).
CC -!- FUNCTION: May play a role in cell-cell or cell-ligand interactions
CC during synaptogenesis and other events in the brain.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
CC domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; M11749; AAG1180.1; -; Genomic DNA.
DR EMBL; AF261093; AAG13904.1; -; mRNA.
DR EMBL; AL161958; CAH82306.1; -; mRNA.
DR EMBL; BC005175; AAH05175.1; -; mRNA.
DR EMBL; BC065559; AAH65559.1; -; mRNA.
DR EMBL; S59749; AAB26353.2; -; mRNA.
DR F1R; A02106; TDHU.
DR F1R; T47130; T47130.
DR Ensemble; ENSG00000154096; Homo sapiens.
DR HGNC; HGNC:11801; THY1.
DR H-InvDB; HIX0010195; -.
DR MIM; 188230; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF000447; ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Glycoprotein; GPI-anchor; Immunoglobulin domain; Lipoprotein;
KW Membrane; Signal; T-cell.
FT SIGNAL 1 19
FT CHAIN 20 130 Thy-1 membrane glycoprotein.
FT PROPEP 131 161 Removed in mature form.
FT DOMAIN 20 126 Ig-like V-type.
FT LIPID 130 130 GPI-anchor amidated cysteine.
FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 79 79 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 119 119 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 139 139 By similarity.
FT DISULFID 28 130 By similarity.
FT DISULFID 38 104 LT -> AP (in Ref. 5).
FT CONFLICT 54 55 N -> H (in Ref. 1).
FT CONFLICT 85 85 N -> H (in Ref. 1).
SQ SEQUENCE 161 AA; 17935 MW; 2B6796DA8E7454B CRC64;

Query Match 70.1%; Score 424; DB 1; Length 161;
Best Local Similarity 73.9%; Pred. No. 8.8e-37;
Matches 88; Conservative 3; Mismatches 12; Indels 16; Gaps 3;

QY 1 QVSRGQKVTSLTACLVDSLRDCHRENTSSSNVYMHFSLTRTKKHVLFGTID-PADSY 59
DB 15 QVSRGQKVTSLTACLVDSLRDCHRENTSSSPQIYEFSLTRTKKHVLFGTVGPEHTY 74
QY 60 TS-----YNQNF-----KDEGTYTCALHSHGSPPISSQNVTVLRDLKLVKCEGV 103
DB 75 RSRNTFTSKYNKVKVLSAFTSKDEGTYTCALHSHGSPPISSQNVTVLRDLKLVKCEGI 133

RESULT 2
Q5R508_PONPY PRELIMINARY; PRT; 161 AA.
ID Q5R508_PONPY
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AC Q5R508;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp459C1015.
GN Name=DKFZp459C1015;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German cDNA Consortium;
RA Bloeker H., Boecher M., Brandt P., Mewes H.W., Weill B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR861077; CAH93158.1; -; mRNA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 161 AA; 17963 MW; 2B6791DD8CB0401B CRC64;

Query Match 69.1%; Score 418; DB 2; Length 161;
Best Local Similarity 72.3%; Pred. No. 3.8e-36;
Matches 86; Conservative 5; Mismatches 12; Indels 16; Gaps 3;

QY 1 QVSRGQKVTSLTACLVDSLRDCHRENTSSSNVYMHFSLTRTKKHVLFGTID-PADSY 59
DB 15 QVSRGQKVTSLTACLVDSLRDCHRENTTSPQIYEFSLTRTKKHVLFGTVGPEHTY 74
QY 60 TS-----YNQNF-----KDEGTYTCALHSHGSPPISSQNVTVLRDLKLVKCEGV 103
DB 75 RSRNTFTSKYNKVKVLSAFTSKDEGTYTCALHSHGSPPISSQNVTVLRDLKLVKCEGI 133

RESULT 3
THY1_MACMU
ID THY1_MACMU STANDARD; PRT; 161 AA.
AC 062643;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CD90
DE antigen).
DE Name=THY1;
GN Macaca mulatta (Rhesus macaque).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopitheciniae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RA Margulies B.J., Clements J.E.;
RT "Rhesus macaque CD90.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May play a role in cell-cell or cell-ligand interactions
CC during synaptogenesis and other events in the brain.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
CC domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
ID Q5R508_PONPY PRELIMINARY; PRT; 161 AA.
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DR EMBL; U93310; AAC05640.1; -, mRNA.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Glycoprotein; GPI-anchor; Immunoglobulin domain; Lipoprotein;
KW Membrane; Signal; T-cell.
FT SIGNAL 1 19
FT CHAIN 20 130
FT PROPEP 131 161
FT DOMAIN 20 126
FT LIPID 130 130
FT CARBOHYD 42 42
FT CARBOHYD 79 79
FT CARBOHYD 119 119
FT CARBOHYD 139 139
FT DISULPID 28 130
FT DISULPID 38 104
SQ SEQUENCE 161 AA; 18011 MW; 326B135498BA401B CRC64;

Query Match 68.9%; Score 417; DB 1; Length 161;
Best Local Similarity 72.3%; Pred. No. 4.9e-36;
Matches 86; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

QY 1 QVSRGQKVTSLTACLDVQSLRDLCHRENTSSSNYMHFSLTRTKKHVLFGTID-PADSY 59
DB 15 QVSRGQKVTSLTACLDVQSLRDLCHRENTSSPIQYEFSLTRTKKHVLFGTGVPEHTY 74

QY 60 TS-----YNQ-----NFKDEGTYTCALHSHGSPPISSQNTVTLRDLKLVKCEGV 103
DB 75 RSRNTFTSKYNMKVLYLSAFTKXDEGTYTCXHLHSHGSPPISSQNTVTLRDLKLVKCEGI 133

RESULT 4
ID Q59GA0 HUMAN PRELIMINARY; PRT; 145 AA.
AC Q59GA0;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Thy-1 cell surface antigen variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno P.R.;
RT "None Title.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB209209; BAD92446.1; -, mRNA.
FT NON TER 1
SQ SEQUENCE 145 AA; 15904 MW; 9DA4BC208DCD5766 CRC64;

Query Match 62.3%; Score 377; DB 2; Length 145;
Best Local Similarity 72.7%; Pred. No. 7.5e-32;
Matches 80; Conservative 2; Mismatches 12; Indels 16; Gaps 3;

QY 1 QVSRGQKVTSLTACLDVQSLRDLCHRENTSSSNYMHFSLTRTKKHVLFGTID-PADSY 59
DB 31 QVSRGQKVTSLTACLDVQSLRDLCHRENTSSSPIQYEFSLTRTKKHVLFGTGVPEHTY 90

QY 60 TS-----YNQNF-----KDEGTYTCALHSHGSPPISSQNTVTLR 94
DB 91 RSRNTFTSKYNMKVLYLSAFTSKDEGTYTCALHSHGSPPISSQNTVTLR 140

RESULT 5
Q9WUR5_CAVPO PRELIMINARY; PRT; 161 AA.
AC Q9WUR5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Thy-1 protein precursor.
GN Name=Thy-1;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathia; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Schaefer H., Burger R., Otto A., Bartels T.;
RT "Characterization and cloning of guinea pig Thy-1.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ238589; CAB44008.1; -, mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 19
FT CHAIN 20 161
FT SEQUENCE 161 AA; 17995 MW; 241461D901F80B1B CRC64;

Query Match 54.9%; Score 332; DB 2; Length 161;
Best Local Similarity 60.5%; Pred. No. 5e-27;
Matches 72; Conservative 10; Mismatches 21; Indels 16; Gaps 3;

QY 1 QVSRGQKVTSLTACLDVQSLRDLCHRENTSSSNYMHFSLTRTKKHVLFGTID-PADSY 59
DB 15 QVSRGQKVTSLTACLDVQSLRDLCHRENTTPIQYEFSLTRTKKHVLFGTGVPEHAY 74

QY 60 TS-----YNQNF-----KDEGTYTCALHSHGSPPISSQNTVTLRDLKLVKCEGV 103
DB 75 RSRNTFTSKYNMKVLYLSAFTKDEGTYTCXHLHSHGSPPISSQNTVTLRDLKLVKCEGI 133

RESULT 6
THY1_MOUSE
ID THY1_MOUSE STANDARD; PRT; 162 AA.
AC P01831;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CD90) (CD90 antigen).
GN Name=Thyl; Synonyms=Thy-1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=85115360; PubMed=2857501;
RX Seki T., Chang H.-C., Moriuchi T., Denome R., Ploegh H., Silver J.;
RT "A hydrophobic transmembrane segment at the carboxyl terminus of thy-1.";
RL Science 227:649-651(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE (THY-1.2 ALLOTYPES).
RC STRAIN=BALB/c;
RX MEDLINE=86055760; PubMed=2866091;
RA Gignere V., Isobe K.-I., Grosveld F.;
RT "Structure of the murine Thy-1 gene.";
RL EMBO J. 4:2017-2024(1985).
RN [3]
RP NUCLEOTIDE SEQUENCE (THY-1.2 ALLOTYPES).
RN
```

RX MEDLINE=85216583; PubMed=2582427;
RA Chang H.-C., Seki T., Moriuchi T., Silver J.;
RT "Isolation and Characterization of mouse Thy-1 genomic clones.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3819-3823(1985).
RN [4]
RP NUCLEOTIDE SEQUENCE (THY-1.2 ALLOTYPED).
RX MEDLINE=86113437; PubMed=2868059;
RA Ingraham H.A., Lawless G.M., Evans G.A.;
RT "The mouse Thy-1.2 glycoprotein gene: complete sequence and
RT identification of an unusual promoter.";
RL J. Immunol. 136:1482-1489(1986).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Olfactory epithelium;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Tomlinson P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP PROTEIN SEQUENCE OF 20-131.
RX MEDLINE=82199396; PubMed=6177036;
RA Williams A.F., Gagnon J.;
RT "Neuronal cell Thy-1 glycoprotein: homology with immunoglobulin.";
RL Science 216:696-703(1982).
CC -!- FUNCTION: May play a role in cell-cell or cell-ligand interactions
CC during synaptogenesis and other events in the brain.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- POLYMORPHISM: There are two major alleles, Thy-1.2 and Thy-1.1.
CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
CC domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; X03151; CAA26930.1; -; Genomic DNA.
CC EMBL; X02771; CAA26548.1; -; Genomic DNA.
CC EMBL; X02772; CAA26549.1; ALT_SEQ; Genomic DNA.
CC EMBL; M10246; AAA40440.1; -; Genomic DNA.
CC EMBL; M11660; AAA40441.1; -; Genomic DNA.
CC EMBL; M12379; AAA40443.1; -; Genomic DNA.
CC EMBL; BC054436; AAH54436.1; -; mRNA.
CC F01; A94278; IDMS.
CC Ensembl; ENSMUSG00000032011; Mus musculus.
CC MGI; MGI:98747; Thy1.
CC GO; GO:0009897; C:external side of plasma membrane; IDA.
CC InterPro; IPR007110; IG-Like.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Direct protein sequencing; Glycoprotein; GPI-anchor;
KW Immunoglobulin domain; Lipoprotein; Membrane; Polymorphism;
KW Pyroglutamate carboxylic acid; Signal; T-cell.
FT SIGNAL 1 19
FT CHAIN 20 131 Thy-1 membrane glycoprotein.

FT PROPEP 132 162 Removed in mature form.
FT DOMAIN 20 127 Ig-like V-type.
FT MOD_RES 20 20 Pyrrolidone carboxylic acid.
FT LIPID 131 131 GPI-anchor amidated cysteine.
FT CARBOHYD 42 42 N-linked (GlcNAc...).
FT CARBOHYD 94 94 N-linked (GlcNAc...).
FT CARBOHYD 118 118 N-linked (GlcNAc...).
FT DISULFID 28 131
FT DISULFID 38 105
FT VARIANT 108 180
SQ SEQUENCE 162 AA; 18080 MW; 397BF7D3A9F2C77B CRC64;
Query Match 48.2%; Score 291.5; DB 1; Length 162;
Best Local Similarity 55.8%; Pred. No. 9.9e-23;
Matches 67; Conservative 13; Mismatches 23; Indels 17; Gaps 5;
QY 1 QVSRGQKVTSLTACLVQDSLRDCHENTSSNYWMH-FSLTRTKKHLVFGTID-PADS 58
Db 15 QVSRGQKVTSLTACLVQDSLRDCHENTSSNYWMH-FSLTRTKKHLVFGTID-PADS 74
QY 59 Y-----TSYQ-----NF--KDEGYTCALHHSGHSPPISSQNTVTLRDLKVKCEGV 103
Db 75 YRSRVTLNQPIYIKVLTLANFTTKDEGYFCELVQSGANPMSSNKSISVYRDLKVKCGI 134
RESULT 7
QY3YX2 MOUSE PRELIMINARY; PRT; 162 AA.
ID Q53YX2 MOUSE PRELIMINARY; PRT; 162 AA.
AC Q53YX2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE CD90.1.
GN Name=Thy1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Delaite E., Jean L., Tron F., Boyer O.;
RT "A single amino acid substitution confers CD90.1 (Thy1.1) allotype
RT specificity.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY445633; AARI7087.1; -; mRNA.
DR Ensembl; ENSMUSG00000032011; Mus musculus.
DR MGI; MGI:98747; Thy1.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR InterPro; IPR007110; IG-Like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 162 AA; 18108 MW; 6978F4D3A9F2C530 CRC64;
Query Match 48.2%; Score 291.5; DB 2; Length 162;
Best Local Similarity 55.8%; Pred. No. 9.9e-23;
Matches 67; Conservative 13; Mismatches 23; Indels 17; Gaps 5;
QY 1 QVSRGQKVTSLTACLVQDSLRDCHENTSSNYWMH-FSLTRTKKHLVFGTID-PADS 58
Db 15 QVSRGQKVTSLTACLVQDSLRDCHENTSSNYWMH-FSLTRTKKHLVFGTID-PADS 74
QY 59 Y-----TSYQ-----NF--KDEGYTCALHHSGHSPPISSQNTVTLRDLKVKCEGV 103
Db 75 YRSRVTLNQPIYIKVLTLANFTTKDEGYFCELVQSGANPMSSNKSISVYRDLKVKCGI 134
RESULT 8
ID THY1_RAT STANDARD; PRT; 161 AA.
FT CHAIN 20 131

AC P01830;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CD90) (CD90 antigen)
GN Name=Thy1; Synonyms=Thy-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86005549; PubMed=2864289;
RA Seki T., Chang H.-C., Moriuchi T., Denome R., Silver J.;
RT "Thy-1: a hydrophobic transmembrane segment at the carboxyl terminus";
RL Fed. Proc. 44:2865-2869 (1985).
RN [2]
RN NUCLEOTIDE SEQUENCE OF 1-122.
RX MEDLINE=83115223; PubMed=6130472;
RA Moriuchi T., Chang H.-C., Denome R., Silver J.;
RT "Thy-1 cDNA sequence suggests a novel regulatory mechanism.";
RL Nature 301:80-82 (1983).
RN [3]
RN NUCLEOTIDE SEQUENCE OF 20-161.
RX MEDLINE=85111162; PubMed=2857477;
RA Seki T., Moriuchi T., Chang H.-C., Denome R., Silver J.;
RT "Structural organization of the rat thy-1 gene";
RL Nature 313:485-487 (1985).
RN [4]
RN NUCLEOTIDE SEQUENCE OF 20-161.
RX MEDLINE=85051865; PubMed=6149956; DOI=10.1016/0014-5793(84)81250-8;
RA Moriuchi T., Silver J.;
RT "Rat Thy-1 antigen has a hydrophobic segment at the carboxyl terminus";
RL FEBS Lett. 178:105-108 (1984).
RN [5]
RN PROTEIN SEQUENCE OF 20-130.
RX MEDLINE=82068190; PubMed=6118137;
RA Campbell D.G., Gagnon J., Reid K.B.M., Williams A.F.;
RT "Rat brain Thy-1 glycoprotein. The amino acid sequence, disulphide bonds and an unusual hydrophobic region.";
RL Biochem. J. 195:15-30 (1981).
RN [6]
RN STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=87275814; PubMed=2886334;
RA Parekh R.B., Tee A.G.D., Dwek R.A., Williams A.F., Rademacher T.W.;
RT "Tissue-specific N-glycosylation, site-specific oligosaccharide patterns and lentil lectin recognition of rat Thy-1.";
RL EMBO J. 6:1233-1244 (1987).
CC -1- FUNCTION: May play a role in cell-cell or cell-ligand interactions during synaptogenesis and other events in the brain.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- TISSUE SPECIFICITY: Abundant in lymphoid tissues.
CC -1- PTM: Glycosylation is tissue specific. Sialylation of N-glycans at Asn-93 in brain and at Asn-42, Asn-93 and Asn-117 in thymus.
CC -1- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
CC ENBL; X03152; CAA26931.1; -; Genomic DNA.
DR ENBL; X03150; CAA26929.1; -; mRNA.
DR ENBL; X02002; CAA26033.1; -; Genomic DNA.
DR ENBL; M18002; AAA42243.1; -; mRNA.
DR ENBL; M10666; AAA42242.1; -; mRNA.
PIR; B45909; TDRT.

DR Ensembl; ENSRNOG00000006604; Rattus norvegicus.
DR RGD; 3860; Thy1.
DR GO; GO:000986; C:cell surface; TAS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00409; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Glycoprotein; GPI-anchor;
KW Immunoglobulin domain; Lipoprotein; Membrane;
KW Pyroglutamate carboxylic acid; Sialic acid; Signal; T-cell.
FT SIGNAL 1 19
FT CHAIN 20 130
FT PROPEP 131 161
FT DOMAIN 20 126
FT MOD_RES 20 20
FT LIPID 130 130
FT CARBOHYD 42 42
FT CARBOHYD 42 42
FT CARBOHYD 93 93
FT CARBOHYD 117 117
FT CARBOHYD 117 117
FT DISULFID 28 130
FT DISULFID 38 104
FT CONFLICT 71 71
FT SEQUENCE 161 AA; 18172 MW; 3285748F3C2C5AB2 CRC64;
SQ
Query Match 46.3%; Score 280; DB 1; Length 161;
Best Local Similarity 50.4%; Pred. No. 1.6e-21;
Matches 60; Conservative 16; Mismatches 27; Indels 16; Gaps 3;
QY 1 QVSRGQKVISLACLVDSRLDCHRENTSSSNWYHFSLTRETKKHVLEGTID-PADSY 59
DB 15 QMSRGQRVISLACLVDSRLDCHRENTSSSNWYHFSLTRETKKHVLEGTID-PADSY 74
QY 60 TS-----YQNQF-----KDEGTTCALHSHGSPPISSQNTVTLRDLKLVKCEGV 103
DB 75 RSRVNLFSDFRIKVLTLANFTTKDEGYMCELRVSGQNTSSNKTINIVIRDLKLVKCGI 133
RESULT 9
Q7T252 CHICK
ID Q7T252_CHICK PRELIMINARY; PRT; 160 AA.
AC Q7T252;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE THY1.
GN Name=THY1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RX PubMed=14711516; DOI=10.1016/j.pep.2003.10.011;
RA Mehndiratta P., Walton W.J., Hare J.T., Pulido S., Parthasarathy G., Emmett M.R., Marshall A.G., Logan T.M.;
RT "Expression, purification, and characterization of avian Thy-1 from Leci mammalian and Tns insect cells.";
RL Protein Expr. Purif. 33:274-287 (2004).
DR ENBL; AV230132; AAP31241.1; -; mRNA.
DR Ensembl; ENSGALG00000006751; Gallus gallus.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.

SQ SEQUENCE 160 AA; 18061 MW; 6DC39D8519540CE6 CRC64;

Query Match 31.2%; Score 189; DB 2; Length 160;
Best Local Similarity 35.6%; Pred. No. 7.2e-12;
Matches 42; Conservative 22; Mismatches 38; Indels 16; Gaps 3;

QY 1 QVSRGQKVTSLTACLVDSLRDLCHRENTSSNYMHFSLTRTKKHVLFGTIDPADS-Y 59
15 QAAHQMIRDLGSLGSLVDCRYENKTSNPLTYEFSLTRQ-QKHIIQSTISVENY 74

Db

QY 60 TS-----YNOHF--KDEGTYTCALHSHGSPPISSQNVTVLRDKLVKCEG 102
75 RNRANVTMHKLVCLYLSHFTSDGVMCELCATNDYTGNOIKNITVTKDKLEK 132

Db

RESULT 10

THY1_CHICK STANDARD; PRT; 160 AA.

AC Q07212;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thy-1 membrane glycoprotein precursor (Thy-1 antigen).
GN Name=THY1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 43-55; 59-79 AND 81-101.
RC STRAIN=White leghorn; TISSUE=Brain;
RX MEDLINE=93061794; PubMed=1359371; DOI=10.1016/0169-328X(92)90180-J;
RA Downing B.J., Gooley A.A., Gunning P., Cunningham A., Jeffrey P.L.;
RT "Molecular cloning and primary structure of the avian Thy-1 glycoprotein.";
RL Brain Res. Mol. Brain Res. 14:250-260(1992).
CC -!- FUNCTION: May play a role in cell-cell or cell-ligand interactions during synaptogenesis and other events in the brain.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).
CC -!- TISSUE SPECIFICITY: Forebrain, cerebellum and tectum.
CC -!- DEVELOPMENTAL STAGE: It is detected at embryonic day 4 (E4) in forebrain and tectum. There is an increase in levels between E16 and the first few days post-hatch. During E19 to hatch a rapid reduction in the levels is seen with a general increase in expression in adulthood.
CC -!- PTM: The N-terminus is blocked.
CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like) domain.
CC
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC
CC
CC EMBL; S47368; AAA11899.1; -; mRNA.
CC EMBL; L14924; AAC42216.1; -; mRNA.
CC PIR; A48975; A48975.
CC Ensembl; ENSGALG00000006751; Gallus gallus.
CC InterPro; IPR003599; Ig.
CC SMART; SM00409; IG; 1.
CC Direct protein sequencing; Glycoprotein; GPI-anchor;
KW Immunoglobulin domain; lipoprotein; Membrane;
KW Pyridolone carboxylic acid; Signal; T-cell.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 129 Thy-1 membrane glycoprotein.
FT PROPEP 130 160 Removed in mature form (By similarity).
FT MOD_RES 20 20 Pyridolone carboxylic acid (By similarity).
FT LIPID 129 129 GPI-anchor amidated cysteine (By similarity).
FT

FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 78 78 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 118 118 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 138 138 N-linked (GlcNAc...) (Potential).
FT DISULFID 28 129 By similarity.
FT DISULFID 38 103 By similarity.
FT DISULFID 76 76 R -> F (in Ref. 1; AA sequence).
FT CONFLICT 82 82 H -> I (in Ref. 1; AA sequence).
SQ SEQUENCE 160 AA; 18165 MW; E378D241CC2D4739 CRC64;

Query Match 29.2%; Score 176.5; DB 1; Length 160;
Best Local Similarity 36.2%; Pred. No. 1.5e-10;
Matches 42; Conservative 22; Mismatches 35; Indels 17; Gaps 4;

QY 1 QVSRGQKVTSLTACLVDSLRDLCHRENTSSNYMHFSLTRTKKHVLFGTIDPADS-Y 59
15 QAAHQMIRDLGSLGSLVDCRYENKTSNPLTYEFSLTRQ-QKHIIQSTISVENY 73

Db

QY 60 TS-----YNOHF--KDEGTYTCALHSHGSPPISSQNVTVLRDKLVK 100
74 RNRANVTMHKLVCLYLSHFTSDGVMCELCATNDYTGNOIKNITVTKDKLEK 129

Db

RESULT 11

Q924P9_MOUSE PRELIMINARY; PRT; 143 AA.

AC Q924P9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE V303-D-J-C mu protein (Fragment).
GN Name=V303-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=7523684;
RA Pokkuluri P.R., Southillier F., Li Y., Kuderova A., Lee J., Cygler M.;
RT "Preparation, characterization and crystallization of an antibody Fab fragment that recognizes RNA. Crystal structures of native Fab and three Fab-monomononucleotide complexes.";
RT J. Mol. Biol. 243:283-297(1994).
RL EMBL; AB069916; BAB63932.1; -; mRNA.
DR PIR; PH1160; PH1160.
DR PIR; PH1161; PH1161.
DR PIR; PH1162; PH1162.
DR PIR; S53751; S53751.
DR HSP; P01751; 1A6W.
DR Ensembl; ENSMUSG000000061773; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 143
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 15704 MW; 43CD8C72D52134F6 CRC64;

Query Match 21.8%; Score 132; DB 2; Length 143;
Best Local Similarity 28.2%; Pred. No. 7e-06;
Matches 33; Conservative 12; Mismatches 38; Indels 34; Gaps 2;

QY 19 SLRLDCHRENTSSNYMHFSLTRTKKHVLFGTIDPADSYTSYNQNFK----- 67
17 SVKLSCASGVTFTSYMWQVQRPGQGLEWIGEDPSDSTYNYNQKPKGKATLTVDTSS 76

Db

```
QY 68 -----DEGTYTCALHSHGSPPISSQNVTVLRDK-----LVKCE 101
DR EMBL; AF206025; AAF69323.1; -; mRNA.
Db 77 STAYMQLSLTSDSAVYGCASHYSSDYNGQGTTLTVSSSESQSPFNPVPLVSC 133

RESULT 12
Q91V67_MOUSE
ID Q91V67_MOUSE PRELIMINARY; PRT; 143 AA.
AC Q91V67;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE VH186.2-D-J-C mu protein (V304-D-J-C mu protein) (Fragment).
GN Name=VH186.2-D-J-C mu; Synonyms=V304-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069912; BAB63928.1; -; mRNA.
DR EMBL; AB069914; BAB63930.1; -; mRNA.
DR PIR; S26744; S26744.
DR HSSP; P01751; 1A6W.
DR SMR; Q91V67; 1-129.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM003596; IG_V.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 143
SQ SEQUENCE 143 AA; 15775 MW; 91BC6012B44FE8F CRC64;

Query Match 21.5%; Score 130; DB 2; Length 143;
Best Local Similarity 33.7%; Pred. No. 1.1e-05;
Matches 31; Conservative 15; Mismatches 44; Indels 2; Gaps 1;

QY 19 SRLDCRHEHTSSNYMHFSLTRTKKHLVFGTIDPADSYTSYQNFKDEGTYTCALHH 78
Db 17 SVKLSCKASGYSTPTSYMHVWVKRPGQGLEWIGVIDPSDSTYNQKFKGKATLTVDTS 76

QY 79 SGHSPPISSQNVTVLRDKLVKCEGVYRYFD 110
Db 77 STAYMQLSS--LTSEDSAVYCAPTVDWYFD 106

RESULT 13
Q9JL81_MOUSE
ID Q9JL81_MOUSE PRELIMINARY; PRT; 114 AA.
AC Q9JL81;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
DE OS Mus musculus (Mouse).
DE OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
DE OC Muridae; Murinae; Mus.
DE OX NCBI_TaxID=10090;
DE RN NUCLEOTIDE SEQUENCE.
DE RC STRAIN=BALB/c;
DE RX MEDLINE=20448942; PubMed=1092488;
RX DOI=10.1128/IAI.68.10.5803-5808.2000;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
```

```
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206025; AAF69323.1; -; mRNA.
DR HSSP; P01751; 1NOB.
DR SMR; Q9JL81; 2-114.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM003596; IG_V.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 114
SQ SEQUENCE 114 AA; 12829 MW; 404885FDE68A56F8 CRC64;

Query Match 20.8%; Score 126; DB 2; Length 114;
Best Local Similarity 32.0%; Pred. No. 2.3e-05;
Matches 33; Conservative 11; Mismatches 41; Indels 18; Gaps 2;

QY 19 SRLDCRHEHTSSNYMHFSLTRTKKHLVFGTIDPADSYTSYQNFKDEGTYTCALHH 78
Db 9 SVKLSCKASGYSTPTSYMHVWVKRPGQGLEWIGVIDPSDSTYNQKFKGKATLTVDTS 64

QY 79 SGHSPPISSQNVTVLRDKLVKCEGVYRYFD 111
Db 65 ----DKSSSTAYMQLSSPTSEDSAVYCARSNYGSLLYFYD 103

RESULT 14
Q924R8_MOUSE
ID Q924R8_MOUSE PRELIMINARY; PRT; 146 AA.
AC Q924R8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RX PubMed=3135311;
RA Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the GAT idiotype cascade. Immunization of
RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
RT specific V genes as the original antigen.";
RL J. Immunol. 141:779-784(1988).
DR EMBL; AB067781; BAB63266.1; -; mRNA.
DR PIR; F28833; F28833.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
```


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OM protein - protein search, using sw model

Run on: December 6, 2005, 10:32:12 ; Search time 103.652 Seconds
(without alignments)
470.529 Million cell updates/sec

Title: US-10-611-655-4
Perfect score: 605
Sequence: 1 QVSRQKVTSLTACLVDQSL.....VLRDKLVKCEGVYRYFYDY 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	605	100.0	111	9	Adw10186 Thy-1 bas
2	424	70.1	161	7	Adp65208 Human Thy
3	424	70.1	161	8	Ab084755 Human can
4	424	70.1	161	9	Adz13572 Human can
5	424	70.1	161	9	Adz13574 Human can
6	424	70.1	161	9	Adz13570 Human can
7	424	70.1	165	3	Aab43939 Human can
8	424	70.1	165	4	Aag73850 Human col
9	422	69.8	161	5	Abb90744 Human Tum
10	422	69.8	161	6	Abu54451 Human Tum
11	419	69.3	368	2	Aay31789 Human Thy
12	402.5	66.5	162	9	Adw10183 Chimeric
13	398	65.8	176	9	Adw10192 Chimeric
14	398	65.8	334	9	Adw10190 Erythrope
15	398	65.8	334	9	Adw10188 Chimeric
16	395	65.3	119	2	Aay31787 Human Thy
17	377	62.3	150	8	Adk98542 Human imm
18	291.5	48.2	162	5	Abb90786 Mouse Tum
19	291.5	48.2	162	6	Abu54493 Mouse Tum
20	291.5	48.2	162	8	Ab084754 Murine ca
21	291.5	48.2	162	9	Adz13567 Murine ca
22	291	48.1	171	4	Abg19538 Novel hum
23	280	46.3	161	2	Aaw53480 Rat Thy-1
24	277	45.8	368	2	Aay31788 Rat Thy-1

25	264.5	43.7	114	7	Adf12417	Adf12417	Mouse Thy
26	264.5	43.7	114	8	Adg39435	Adg39435	Mouse Thy
27	256	42.3	119	2	Aay31786	Aay31786	Rat Thy-1
28	242.5	40.1	105	3	Aag00166	Aag00166	Human sec
29	198	32.7	125	2	Aay27074	Aay27074	Monoclonal
30	186.5	30.8	124	9	Adw10184	Adw10184	Human ant
31	162	26.8	51	4	Abg19536	Abg19536	Novel hum
32	143.5	23.7	119	8	Adp79380	Adp79380	Thyrotrop
33	143.5	23.7	124	8	Adp79384	Adp79384	Thyrotrop
34	131	21.7	309	4	Aar70841	Aar70841	SNV-env 1
35	129.5	21.4	118	8	Adu39962	Adu39962	Antibody
36	128.5	21.2	117	1	Aap80148	Aap80148	Biosynthe
37	128.5	21.2	117	1	Aab62295	Aab62295	Sequence
38	128	21.2	98	8	Ado58553	Ado58553	GAP gene
39	128	21.2	116	8	Adm33983	Adm33983	Anti-Nogo
40	128	21.2	116	9	Ady34450	Ady34450	Nogo rece
41	127.5	21.1	117	9	Ady60815	Ady60815	Hybrid pr
42	126.5	20.9	117	8	Adf77173	Adf77173	Anti-VAP-
43	125.5	20.7	119	2	Aar79863	Aar79863	Anti-EGFR
44	125	20.7	117	2	Aaw00831	Aaw00831	Variable
45	125	20.7	117	2	Aaw19017	Aaw19017	Anti-huma

ALIGNMENTS

RESULT 1
ADW10186
ID ADW10186 standard; protein; 111 AA.
XX
AC ADW10186;
XX
DT 24-MAR-2005 (first entry)
XX
DE Thy-1 based ThyOx non-immunoglobulin binding polypeptide, SEQ ID 4.
XX non-immunoglobulin binding polypeptide; selective binding; ThyOx.
XX Synthetic.
XX US2004266993-A1.
XX 30-DEC-2004.
XX 30-JUN-2003; 2003US-00611655.
XX 30-JUN-2003; 2003US-00611655.
XX (EVAN/) EVANS G A.
XX Evans GA;
XX WPI; 2005-047648/05.
PT New chimeric non-immunoglobulin binding polypeptide comprises immunoglobulin-like domain containing scaffold and exhibits selective binding activity, for producing non-immunoglobulin binding polypeptides with selective binding activity.
PT Disclosure; SEQ ID NO 4; 45pp; English.
PS The invention relates to a novel chimeric non-immunoglobulin binding polypeptide. The polypeptide comprises an immunoglobulin-like domain containing scaffold with two or more solvent exposed loops containing a different complementarity-determining region (CDR) from a parent antibody inserted into each of the loops and exhibiting selective binding activity toward a ligand bound by the parent antibody. The invention further comprises: a chimeric ThyOx binding polypeptide, comprising one or more altered immunoglobulin-like domain loop regions of a ThyOx family polypeptide or at least one immunoglobulin-like domain containing scaffold derived from a Thyox family polypeptide, and a heterologous binding polypeptide exhibiting selective binding activity toward a non-ThyOx ligand, and a nucleic acid encoding the non-immunoglobulin or ThyOx

CC binding polypeptide above. The chimeric non-immunoglobulin binding
 CC polypeptide is useful for producing non-immunoglobulin binding
 CC polypeptides having selective binding activity toward a predetermined
 CC molecule. This sequence represents a Thyox non-immunoglobulin binding
 CC polypeptide of the invention.

XX SQ Sequence 111 AA;

Query Match 100.0%; Score 605; DB 9; Length 111;
 Best Local Similarity 100.0%; Pred. No. 1.8e-57;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVSRGQKVTSLTACLVDSLRDCHRENTSSNYMHFSLTRETCKHVLFGTIDPADSYT 60

Db 1 QVSRGQKVTSLTACLVDSLRDCHRENTSSNYMHFSLTRETCKHVLFGTIDPADSYT 60

QY 61 SYNQNFDEGTYTCALHSHGSPPISSQNVTVLRDCLKVCEGVYRYFYDY 111

Db 61 SYNQNFDEGTYTCALHSHGSPPISSQNVTVLRDCLKVCEGVYRYFYDY 111

RESULT 2

ID ADP65208 standard; protein; 161 AA.

XX AC ADP65208;

XX DT 12-AUG-2004 (first entry)

XX DE Human Thy-1 cell surface antigen, Thy-1 T-cell antigen.

XX KW autoimmune disease; arthritis; gene expression analysis;
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
 KW antihypertensive; osteoporosis; antihypertensive; antirheumatic;
 KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; human.

XX OS Homo sapiens.

XX PN WO2003072827-A1.

XX PD 04-SEP-2003.

XX PF 31-OCT-2002; 2002WO-US035433.

XX PR 31-OCT-2001; 2001US-0336220P.

XX PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX PI Hirsch R, Thorton SL;

XX DR WPI; 2003-712740/67.

XX DR GENBANK; NP_006279.

XX PT Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.

XX PS Disclosure; Page; 56pp; English.

XX CC The invention relates to a novel method for diagnosing and analysing
 CC autoimmune disease or arthritis. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritis in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or

CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antihypertensive, osteoporosis,
 CC antihypertensive, antirheumatic, antihypertensive, osteoporosis, osteoporosis,
 CC antihypertensive, antirheumatic, antihypertensive, osteoporosis, osteoporosis,
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritis, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This sequence represents a
 CC protein sequence relating to the genes used in the analysis and treatment
 CC of autoimmune diseases or arthritis. Note: This sequence is not shown
 CC in the specification. It has been supplied in an electronic format from
 CC WIPO.

XX SQ Sequence 161 AA;

Query Match 70.1%; Score 424; DB 7; Length 161;
 Best Local Similarity 73.9%; Pred. No. 1.2e-37;
 Matches 88; Conservative 3; Mismatches 12; Indels 16; Gaps 3;

QY 1 QVSRGQKVTSLTACLVDSLRDCHRENTSSNYMHFSLTRETCKHVLFGTID-PADSY 59

Db 15 QVSRGQKVTSLTACLVDSLRDCHRENTSSNYMHFSLTRETCKHVLFGTID-PADSY 74

QY 60 TS-----YNQNF-----KDEGTYTCALHSHGSPPISSQNVTVLRDCLKVCEGV 103

Db 75 RSRTNFTSKYMKVLYLSAFTSKDEGTYTCALHSHGSPPISSQNVTVLRDCLKVCEGV 133

RESULT 3

ABO84755

ID ABO84755 standard; protein; 161 AA.

XX AC ABO84755;

XX DT 18-NOV-2004 (first entry)

XX DE Human cancer-associated protein (CAP) HP07-003.

XX KW Human; cancer-associated protein; CAP; cancer; cytostatic.

XX OS Homo sapiens.

XX PN WO2004058146-A2.

XX PD 15-JUL-2004.

XX PF 15-DEC-2003; 2003WO-US040081.

XX PR 17-DEC-2002; 2002US-00322281.

XX PA (SAGR-) SAGRES DISCOVERY INC.

XX PI Morris DW, Malandro MS;

XX DR WPI; 2004-499109/47.

XX DR N-PSDB; ABD33081.

XX PT Novel human cancer associated protein encoded within open reading frame
 PT of cancer associated gene, useful as targets for diagnosing cancer.

XX PS Claim 18; SEQ ID NO 20; 182pp; English.

XX CC The invention relates to cancer-associated proteins (CAP) and the cancer-
 CC associated (CA) nucleic acids encoding them. The invention also relates
 CC to a method for treating cancers involving administering to a patient an
 CC inhibitor of CAP, and a method of screening for anticancer activity in a
 CC potential drug involving providing a cell that expresses a CA gene,
 CC contacting a tissue sample derived from a cancer cell with an anticancer
 CC drug candidate and monitoring the effect of the anticancer drug candidate
 CC on expression of the CA gene. The CAP proteins are useful for detecting

CC cancer associated with expression of a CAP protein in a test cell sample
CC and for screening for a bioactive agent capable of modulating the
CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC cancer, involving determining the expression of a CA nucleic acid in a
CC tissue. This sequence represents a human CAP of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 161 AA;

Query Match	70.1%	Score 424;	DB 8;	Length 161;
Best Local Similarity	73.9%	Pred. No. 1.2e-37;		
Matches 88;	Conservative 3;	Mismatches 12;	Indels 16;	Gaps 3;

Qy	1	QVSRGQKVTSLTACLVQDSRLDCRHNENTSSNTVMHPSLTRETQKGVLFQTTD-PADSY	59
Db	15	QVSRGQKVTSLTACLVQDSRLDCRHNENTSSPIQYEFSLRETQKGVLFQTVGVPEHT	74
Qy	60	TS-----YNQNF-----KDEGYTTCALAHSGHSPPITSSQNVTTLRDKLVKCEGV	103
Db	75	RSRTNFTSKYMKVLYLSAFTSKDEGYTTCALAHSGHSPPITSSQNVTTLRDKLVKCEGI	133

RESULT 4	
ADZ13572	
ID	ADZ13572 standard; protein; 161 AA.
XX	
XX	ADZ13572;
XX	
DT	16-JUN-2005 (first entry)
XX	
DE	Human cancer-associated protein #329.
XX	
KW	Diagnosis; DNA microarray; microarray; cancer; neoplasm;
KW	cytostatic.
XX	
OS	Homo sapiens.
XX	
PN	WO2005031001-A2.
XX	
PD	07-APR-2005.
XX	
PF	23-SEP-2004; 2004WO-US031617.
XX	
PR	23-SEP-2003; 2003US-00669920.
XX	
PA	(CHIR) CHIRON CORP.
XX	
PI	Morris DW, Malandro MS;
XX	
DR	WPI; 2005-273395/28.
XX	
XX	N-PSDB; ADZ13571.
XX	
PT	Nucleic acid array useful for detecting cancer associated nucleic
PT	acid probes.
XX	
PS	comprises two or more nucleic acid probes.
XX	
PS	Disclosure; SEQ ID NO 1092; 198pp; English.

The invention relates to a nucleic acid array for detecting a cancer associated (CA) nucleic acid, comprising two or more nucleic acid probes. The invention also relates to a peptide array comprising two or more isolated polypeptides encoded by a CA nucleic acid sequence, a compound that binds to a polypeptide, an isolated antibody or its fragment which binds to a polypeptide, which is prepared by immunizing a host animal with a composition comprising the polypeptide or its antigen binding fragment and collecting cells from the host expressing antibodies against the antigen or its antigen binding fragment, a composition comprising the antibody and a carrier, a method of screening for anticancer activity, a method of detecting a CA nucleic acid, a method of diagnosing cancer, a method of treating cancer and a method of inhibiting expression of a CA nucleic acid in a cell. The CA nucleic acids are useful for detecting CA nucleic acids. The antibody is useful for detecting the presence or

CC absence of cancer cells in an individual which involves contacting cells
CC from the individual with the antibody and detecting a complex of a CA
CC protein from the cancer cells and the antibody, where the detection of CA
CC the complex correlates with the presence of cancer cells in the
CC individual. The composition is useful for inhibiting growth of cancer
CC cells in an individual or for delivering a therapeutic agent to cancer
CC cells in an individual. The invention is also useful for diagnosing
CC cancer, for treating cancer and for inhibiting expression of a CA gene in
CC a cell. This sequence represents a human cancer-associated protein of the
CC invention.

```

SQ      Sequence 161 AA;

Query Match      70.1%; Score 424; DB 9; Length 161;
Best Local Similarity 73.9%; Pred. No. 1.2e-37;
Matches 88; Conservative 3; Mismatches 12; Indels 16; Gaps 3

Qy      1  QVSRGQKVTSLTACLVDQSLRDCRHEHNTSSNNTWMHPSLTRETKKHVLFGTID-PADSY 59
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      15  QVSRGQKVTSLTACLVDQSLRDCRHEHNTSSSPIQYEPSLTRETKKHVLFGTVGPEHTY 74

Qy      60  TS-----YQNPF-----KDEGTYTCALHHSGHSPPISSQNVTVLRLDKLVKCEGV 103
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      75  RSRNTFTSKTNMKVLYLSAFTSKDEGTYTCALHHSGHSPPISSQNVTVLRLDKLVKCEGI 133

```

RESULT 5
ADZ13574
ID ADZ13574 standard; protein; 161 AA.
XX
AC AC ADZ13574;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human cancer-associated protein #330.
XX
KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
XX cytostatic.
XX
OS Homo sapiens.
XX
PN WC2005031001-A2.
XX
PD 07-APR-2005.
XX
PF 23-SEP-2004; 2004WO-US031617.
XX
PR 23-SEP-2003; 2003US-00669920.
XX
PA (CHIR) CHIRON CORP.
XX
PI Morris DW, Malandro MS;
XX
WPI; 2005-273395/28.
DR N-PSDB; ADZ13573.
XX
PT Nucleic acid array useful for detecting cancer associated nucleic acid,
PS comprises two or more nucleic acid probes.
XX
PP Disclosure; SEQ ID NO 1094; 198pp; English.

The invention relates to a nucleic acid array for detecting a cancer associated (CA) nucleic acid, comprising two or more nucleic acid probes. The invention also relates to a peptide array comprising two or more isolated polypeptides encoded by a CA nucleic acid sequence, a compound that binds to a polypeptide, an isolated antibody or its fragment which binds to a polypeptide, which is prepared by immunizing a host animal with a composition comprising the polypeptide or its antigen binding fragment and collecting cells from the host expressing antibodies against the antigen or its antigen binding fragment, a composition comprising the antibody and a carrier, a method of screening for anticancer activity, a method of detecting a CA nucleic acid, a method of diagnosing cancer, a method of treating cancer and a method of inhibiting expression of a CA

CC AAC77607 to AAC78448 encode the human cancer associated proteins given in
CC AAB43398 to AAB44239. The proteins can have activities based on the
CC tissues and cells the genes are expressed in. Example of activities
CC include: cytostatic; proliferative; vulnarary; immunomodulator;
CC antidiabetic; antiaschmatic; antirheumatic; antiarthritic;
CC antinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC dermatologic; neuroprotective; cardiant; thrombolytic; coagulant;
CC neotropic; vasotropic; antipsoriatic and antiangiogenic. The
CC polynucleotides and polypeptides can be used for preventing, treating or
CC ameliorating medical conditions and diagnosing pathological conditions.
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC the present invention may be used to treat immune disorders by activating
CC or inhibiting the proliferation, differentiation or mobilisation of
CC immune cells, to treat disorders of haematopoietic cells, autoimmune
CC disorders, allergic reactions, graft versus host disease and organ
CC rejection, modulate haemostatic or thrombolytic activity, modulate
CC inflammation, cancers, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies,
CC agonists and antagonists may be also be used in drug screens. AAC78449 to
CC AAC78457 and AAB44240 represent sequences used in the exemplification of
CC the present invention
XX

Query Match 70.1%; Score 424; DB 3; Length 165;
Best Local Similarity 73.9%; Pred. No. 1.3e-37;
Matches 88; Conservative 3; Mismatches 12; Indels 16; Gaps 3;
SQ Sequence 165 AA;

QY 1 QVSRGQKVTSLTACLVDSLRDLCRHENTSSSNYMHFSLTRTKKHVLFGTID-PADSY 59
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : :
19 QVSRGQKVTSLTACLVDSLRDLCRHENTSSSPIQYEFSLTRTKKHVLFGTIVGVPHTY 78
QY 60 TS-----YKNQF-----KDEGTYTCALHSHGSHSPPISSQNVTVLRDLKLVKEGV 103
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : :
79 RSRNTFTSKYNMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDLKLVKEGI 137

RESULT 8
AAG73850
ID AAG73850 standard; protein; 165 AA.
XX
AC AAG73850;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO:4614.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome 11.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US026524.
XX
PR 29-SEP-1999; 99US-0157137P.
PR 03-NOV-1999; 99US-0163280P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Barash SC, Birse CB, Rosen CA;
PI WPI; 2001-235357/24.
XX
DR N-PSDB; AAB33281.
XX
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers.
XX
XX Claim 11; Page 6411-6412; 9803pp; English.
XX

CC AAB32943 to AAB37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patients own production of P. Additionally, N may be used
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAB37196 to AAB37204 and AAB77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922
XX
SQ Sequence 165 AA;

Query Match 70.1%; Score 424; DB 4; Length 165;
Best Local Similarity 73.9%; Pred. No. 1.3e-37;
Matches 88; Conservative 3; Mismatches 12; Indels 16; Gaps 3;

QY 1 QVSRGQKVTSLTACLVDSLRDLCRHENTSSSNYMHFSLTRTKKHVLFGTID-PADSY 59
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : :
19 QVSRGQKVTSLTACLVDSLRDLCRHENTSSSPIQYEFSLTRTKKHVLFGTIVGVPHTY 78
QY 60 TS-----YKNQF-----KDEGTYTCALHSHGSHSPPISSQNVTVLRDLKLVKEGV 103
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : :
79 RSRNTFTSKYNMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDLKLVKEGI 137

RESULT 9
ABB90744
ID ABB90744 standard; protein; 161 AA.
XX
AC ABB90744;
XX
DT 30-MAY-2002 (first entry)
XX
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 220.
XX

KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
KW normal endothelial marker; pan-endothelial marker; immunostimulant;
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW psoriasis.

OS Homo sapiens.
XX
PN WO200210217-A2.
XX
PD 07-FEB-2002.
XX
PF 01-AUG-2001; 2001WO-US024031.
XX
PR 02-AUG-2000; 2000US-0222599P.
PR 11-AUG-2000; 2000US-0224360P.
PR 11-APR-2001; 2001US-0282850P.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX St Croix B, Kinzler KW, Vogelstein B;
PI WPI; 2002-291856/33.
XX
DR N-PSDB; ABL92098.
XX

XX An isolated molecule comprising an antibody variable region which
PT specifically binds to an extracellular domain of a tumor endothelial
PT marker (TEM) protein, useful for inhibiting tumor growth.
XX

PS Claim 35; Page 194; 331pp; English.

XX The invention relates to an isolated molecule comprising an antibody

CC variable region which specifically binds to an extracellular domain of a

CC tumour endothelial marker (TEM). The antibodies which bind to TEM

CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM

CC proteins have cytostatic, immunostimulant and antiangiogenic activity.

CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects

CC bearing a vascularised tumour, polycystic kidney disease, diabetic

CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM

CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)

CC are disclosed, as are marker oligonucleotide sequences: tumour

CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal

CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers

CC (PEM) ABL91903-ABL91995

XX Sequence 161 AA;

Query Match 69.8%; Score 422; DB 5; Length 161;

Best Local Similarity 73.3%; Pred. No. 2e-37;

Matches 88; Conservative 3; Mismatches 11; Indels 18; Gaps 3;

QY 1 QVSRGQKVTSLTACLVDSRLDCRHEHTSSNYMHFSLTRETKKHVLFGTID-PADSY 59

DB 15 QVSRGQKVTSLTACLVDSRLDCRHEHTSSPIQYEFSLTRETKKHVLFGTVGVPHTY 74

QY 60 TSYNQNF-----KDEGTYTTCALHSHSGHSPPISSQNVTVLRDKLVKCEGV 103

DB 75 RS-RTNFTSKYHMKVLYLSAFTSKDEGTYTTCALHSHSGHSPPISSQNVTVLRDKLVKCEGI 133

RESULT 10

ABUS4451

ID ABUS4451 standard; protein; 161 AA.

XX AC ABUS4451;

XX 12-MAR-2003 (first entry)

DE Human tumour endothelial marker TEM 13.

XX Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;

KW Tumour endothelial marker; normal endothelial marker; PEM;

KW pan-endothelial marker; polycystic kidney disease; psoriasis;

KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;

KW neoangiogenesis; immune response; cytostatic; antidiabetic;

KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic.

XX Homo sapiens.

XX WO200283874-A2.

PN 24-OCT-2002.

XX 10-APR-2002; 2002WO-US008253.

PF 11-APR-2001; 2001US-0282850P.

PR 06-FEB-2002; 2002US-0354262P.

XX (UYJO) UNIV JOHNS HOPKINS.

PA Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;

PI WPI; 2003-093016/08.

DR N-PSDB; ABX72023.

XX New purified human transmembrane protein, designated as tumor endothelial

PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors

PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or

PT psoriasis.

XX Disclosure; Page 206-207; 374pp; English.

XX

CC The present invention relates to a novel method for the isolation of

CC endothelial cells (ECs), and the identification of genes expressed in

CC normal and tumour ECs. Tumour endothelial marker (TEM), normal

CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are

CC identified in human ECs. The human EC marker proteins and the

CC polynucleotide sequences encoding them are useful for detecting,

CC diagnosing or treating tumours as well as polycystic kidney disease,

CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also

CC useful for inhibiting neoangiogenesis or tumour angiogenesis, for

CC inducing an immune response to tumour endothelial cells in a patient, or

CC for identifying candidate drugs for treating tumours. The present

CC sequence represents a human TEM or NEM protein of the invention

XX Sequence 161 AA;

Query Match 69.8%; Score 422; DB 6; Length 161;

Best Local Similarity 73.3%; Pred. No. 2e-37;

Matches 88; Conservative 3; Mismatches 11; Indels 18; Gaps 3;

QY 1 QVSRGQKVTSLTACLVDSRLDCRHEHTSSNYMHFSLTRETKKHVLFGTID-PADSY 59

DB 15 QVSRGQKVTSLTACLVDSRLDCRHEHTSSPIQYEFSLTRETKKHVLFGTVGVPHTY 74

QY 60 TSYNQNF-----KDEGTYTTCALHSHSGHSPPISSQNVTVLRDKLVKCEGV 103

DB 75 RS-RTNFTSKYHMKVLYLSAFTSKDEGTYTTCALHSHSGHSPPISSQNVTVLRDKLVKCEGI 133

RESULT 11

AAV31789

ID AAV31789 standard; protein; 368 AA.

XX AC AAV31789;

XX 17-OCT-2003 (revised)

DT 06-DEC-1999 (first entry)

XX Human Thy-1-human Igg constant region fusion protein.

XX Thy-1; human; Igg; angiogenesis; cancer; tumour; rheumatoid arthritis;

KW atherosclerosis; therapy.

XX Homo sapiens.

OS Chimeric.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Protein /note= "Thy-1 signal peptide"

FT 18..368

FT /note= "Thy-1-Ig fusion, specifically claimed in Claim 8"

XX WO9945951-A2.

PN 16-SEP-1999.

XX 11-MAR-1999; 99WO-US005256.

XX 11-MAR-1998; 98US-00077524.

XX (HARD) HARVARD COLLEGE.

PA (HABE/) HABER C.

XX Haber E, Shaw S, Jain MK, Lee W;

XX WPI; 1999-561618/47.

DR N-PSDB; AAX87980.

XX Inhibiting Thy-1 expression in endothelial cell, useful for inhibiting

PT angiogenesis.

XX Claim 8; Page 46-47; 47pp; English.

XX The present sequence represents a fusion protein, the mature region of

CC

CC which is claimed, comprising the human Thy-1 extracellular region (see
 CC AAY31787) and the constant region (hinge, CH2, CH3) of human IgG1. A
 CC claimed method for inhibiting angiogenesis in a mammal comprises
 CC administering a compound that inhibits Thy-1 associated proliferation of
 CC an endothelial cell. The compound is preferably the extracellular region
 CC of rat or human Thy-1. The method is used in the treatment of a mammal
 CC having a tumour (e.g. by reducing vascularisation), atherosclerosis or
 CC rheumatoid arthritis, the lesions of which may be associated with
 CC neovascularisation (all claimed). Another claimed method for inhibiting
 CC angiogenesis involves administering a Thy-1 antisense nucleic acid or a
 CC Thy-1 specific antibody linked to a cytotoxic agent. A method for
 CC promoting angiogenesis involves administering a compound that increases
 CC Thy-1 expression in an endothelial cell such as a chimeric protein
 CC comprising the Thy-1 extracellular fragment and the constant region of an
 CC immunoglobulin. (Updated on 17-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 368 AA;

Query Match 69.3%; Score 419; DB 2; Length 368;
 Best Local Similarity 73.9%; Pred. No. 1.2e-36;
 Matches 88; Conservative 2; Mismatches 11; Indels 18; Gaps 3;
 QY 1 QVSRGQVTSLSACLVDQSLRLDCRHEHTSSSNYWHFSLTRTKKHVLFGTID-PADSY 59
 DB 15 QVSRGQVTSLSACLVDQSLRLDCRHEHTSSSPIQYEFSLTRTKKHVLFGTIVPEHTY 74
 QY 60 TSYNQNF-----KDEGTYTCALHSHSGHSPPISSQNVTVLRLDKLVKCEG 102
 DB 75 RS-RTNFTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRLDKLVKCEG 132

RESULT 12
 ADW10183
 ID ADW10183 standard; protein; 162 AA.
 XX
 AC ADW10183;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE Human Thy-1 protein.
 XX
 KW non-immunoglobulin binding polypeptide; selective binding; Thy-1.
 XX
 OS Homo sapiens.
 XX
 PN US2004266993-A1.
 XX
 PD 30-DEC-2004.
 XX
 PF 30-JUN-2003; 2003US-00611655.
 XX
 PR 30-JUN-2003; 2003US-00611655.
 XX
 PA (EVAN/) EVANS G A.
 XX
 PI Evans GA;
 XX
 DR WPI; 2005-047648/05.
 XX

PT New chimeric non-immunoglobulin binding polypeptide comprises
 PT immunoglobulin-like domain containing scaffold and exhibits selective
 PT binding activity, for producing non-immunoglobulin binding polypeptides
 PT with selective binding activity.
 XX

PS Disclosure; SEQ ID NO 1; 45pp; English.
 XX
 CC The invention relates to a novel chimeric non-immunoglobulin binding
 CC polypeptide. The polypeptide comprises an immunoglobulin-like domain
 CC containing scaffold with two or more solvent exposed loops containing a
 CC different complementarity-determining region (CDR) from a parent antibody
 CC inserted into each of the loops and exhibiting selective binding activity
 CC toward a ligand bound by the parent antibody. The invention further
 CC comprises a chimeric ThyOx binding polypeptide, comprising one or more

CC altered immunoglobulin-like domain loop regions of a ThyOx family
 CC polypeptide or at least one immunoglobulin-like domain containing
 CC scaffold derived from a ThyOx family polypeptide, and a heterologous
 CC binding polypeptide exhibiting selective binding activity toward a non-
 CC ThyOx ligand; and a nucleic acid encoding the non-immunoglobulin or ThyOx
 CC binding polypeptide above. The chimeric non-immunoglobulin binding
 CC polypeptide is useful for producing non-immunoglobulin binding
 CC polypeptides having selective binding activity toward a predetermined
 CC molecule. This sequence represents a human thy-1 protein of the
 XX
 SQ Sequence 162 AA;

Query Match 66.5%; Score 402.5; DB 9; Length 162;
 Best Local Similarity 71.9%; Pred. No. 2.6e-35;
 Matches 87; Conservative 3; Mismatches 12; Indels 19; Gaps 4;

QY 1 QVSRGQVTSLSACLVDQSLRLDCRHEHTSSSNYWHFSLTRTKKHVLFGTID-PADSY 59
 DB 15 QVSRGQVTSLSACLVDQSLRLDCRHEHTSSSPIQYEFSLTRTKKHVLFGTIVPEHTY 74
 QY 60 TSYNQNF-----KDEGTYTCALHSHSGHSPPISSQNVTVLRLDKLVKCEG 102
 DB 75 RS-RTNFTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRLDKLVKCEG 133
 QY 103 V 103
 DB 134 I 134

RESULT 13
 ADW10192
 ID ADW10192 standard; protein; 176 AA.
 XX
 AC ADW10192;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE Chimeric ThyOx carrier containing glucagon-like peptide 1.
 XX
 KW non-immunoglobulin binding polypeptide; selective binding; ThyOx;
 KW glucagon-like peptide 1; GLP-1.
 XX
 OS Chimeric.
 OS Synthetic.
 XX
 PN US2004266993-A1.
 XX
 PD 30-DEC-2004.
 XX
 PF 30-JUN-2003; 2003US-00611655.
 XX
 PR 30-JUN-2003; 2003US-00611655.
 XX
 PA (EVAN/) EVANS G A.
 XX
 PI Evans GA;
 XX
 DR WPI; 2005-047648/05.
 XX
 N-PSDB; ADW10191.

PT New chimeric non-immunoglobulin binding polypeptide comprises
 PT immunoglobulin-like domain containing scaffold and exhibits selective
 PT binding activity, for producing non-immunoglobulin binding polypeptides
 PT with selective binding activity.
 XX

PS Disclosure; SEQ ID NO 10; 45pp; English.
 XX
 CC The invention relates to a novel chimeric non-immunoglobulin binding
 CC polypeptide. The polypeptide comprises an immunoglobulin-like domain
 CC containing scaffold with two or more solvent exposed loops containing a
 CC different complementarity-determining region (CDR) from a parent antibody
 CC inserted into each of the loops and exhibiting selective binding activity

CC toward a ligand bound by the parent antibody. The invention further
 CC comprises: a chimeric ThyOx binding polypeptide, comprising one or more
 CC altered immunoglobulin-like domain loop regions of a ThyOx family
 CC polypeptide or at least one immunoglobulin-like domain containing
 CC scaffold derived from a ThyOx family polypeptide, and a heterologous
 CC binding polypeptide exhibiting selective binding activity toward a non-
 CC ThyOx ligand; and a nucleic acid encoding the non-immunoglobulin or ThyOx
 CC binding polypeptide above. The chimeric non-immunoglobulin binding
 CC polypeptide is useful for producing non-immunoglobulin binding
 CC polypeptides having selective binding activity toward a predetermined
 CC molecule. This sequence represents a chimeric ThyOx carrier containing
 CC glucagon-like peptide 1 of the invention.
 XX
 SQ Sequence 176 AA;

Query Match 65.8%; Score 398; DB 9; Length 176;
 Best Local Similarity 72.2%; Pred. No. 9e-35;
 Matches 83; Conservative 3; Mismatches 11; Indels 18; Gaps 3;
 QY 6 QKVTSLTACLVDQSLRDCRHSNTSSNNYMHFSLTRTKKHVLFGTID-PADSYTSYNQ 64
 Db 49 QKVTSLTACLVDQSLRDCRHSNTSSNPQYEFSLTRTKKHVLFGTGVPEHTYRS-RT 107
 QY 65 NF-----KDEGTYTCALHSHGSPPISSQNVTVLRDLKLVKCEGV 103
 Db 108 NFKSYHMKVLYLSAFTSKDEGTYTCALHSHGSPPISSQNVTVLRDLKLVKCEGI 162

RESULT 14
 ADM10190
 ID ADM10190 standard; protein; 334 AA.
 XX
 AC ADM10190;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE Erythropoietin protein, named SuperEpo.
 XX non-immunoglobulin binding polypeptide; selective binding; ThyOx;
 KW erythropoietin; SuperEpo.
 XX Chimeric.
 OS Synthetic.
 OS US2004266993-A1.
 PN 30-DEC-2004.
 XX
 PD 30-JUN-2003; 2003US-00611655.
 PF 30-JUN-2003; 2003US-00611655.
 XX
 PR 30-JUN-2003; 2003US-00611655.
 XX (EVAN/) EVANS G A.
 PA
 PI Evans GA;
 XX
 PI WPI; 2005-047648/05.
 DR N-PSDB; ADM10189.
 XX
 PT New chimeric non-immunoglobulin binding polypeptide comprises
 PT immunoglobulin-like domain containing scaffold and exhibits selective
 PT binding activity, for producing non-immunoglobulin binding polypeptides
 PT with selective binding activity.
 XX
 PS Disclosure; SEQ ID NO 8; 45pp; English.

XX The invention relates to a novel chimeric non-immunoglobulin binding
 CC polypeptide. The polypeptide comprises an immunoglobulin-like domain
 CC containing scaffold with two or more solvent exposed loops containing a
 CC different complementarity-determining region (CDR) from a parent antibody
 CC inserted into each of the loops and exhibiting selective binding activity
 CC toward a ligand bound by the parent antibody. The invention further
 CC comprises: a chimeric ThyOx binding polypeptide, comprising one or more
 CC altered immunoglobulin-like domain loop regions of a ThyOx family
 CC polypeptide or at least one immunoglobulin-like domain containing

CC altered immunoglobulin-like domain loop regions of a ThyOx family
 CC polypeptide or at least one immunoglobulin-like domain containing
 CC scaffold derived from a ThyOx family polypeptide, and a heterologous
 CC binding polypeptide exhibiting selective binding activity toward a non-
 CC ThyOx ligand; and a nucleic acid encoding the non-immunoglobulin or ThyOx
 CC binding polypeptide above. The chimeric non-immunoglobulin binding
 CC polypeptide is useful for producing non-immunoglobulin binding
 CC polypeptides having selective binding activity toward a predetermined
 CC molecule. This sequence represents an erythropoietin protein, named
 CC SuperEpo, of the invention.
 XX
 SQ Sequence 334 AA;

Query Match 65.8%; Score 398; DB 9; Length 334;
 Best Local Similarity 72.2%; Pred. No. 2e-34;
 Matches 83; Conservative 3; Mismatches 11; Indels 18; Gaps 3;
 QY 6 QKVTSLTACLVDQSLRDCRHSNTSSNNYMHFSLTRTKKHVLFGTID-PADSYTSYNQ 64
 Db 207 QKVTSLTACLVDQSLRDCRHSNTSSNPQYEFSLTRTKKHVLFGTGVPEHTYRS-RT 265
 QY 65 NF-----KDEGTYTCALHSHGSPPISSQNVTVLRDLKLVKCEGV 103
 Db 266 NFKSYHMKVLYLSAFTSKDEGTYTCALHSHGSPPISSQNVTVLRDLKLVKCEGI 320

RESULT 15
 ADM10188
 ID ADM10188 standard; protein; 334 AA.
 XX
 AC ADM10188;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE Chimeric ThyOx carrier containing erythropoietin.
 XX non-immunoglobulin binding polypeptide; selective binding; ThyOx;
 KW erythropoietin.
 XX Chimeric.
 OS Synthetic.
 OS US2004266993-A1.
 PN 30-DEC-2004.
 XX
 PD 30-JUN-2003; 2003US-00611655.
 PF 30-JUN-2003; 2003US-00611655.
 XX
 PR 30-JUN-2003; 2003US-00611655.
 XX (EVAN/) EVANS G A.
 PA
 PI Evans GA;
 XX
 PI WPI; 2005-047648/05.
 DR N-PSDB; ADM10187.
 XX
 PT New chimeric non-immunoglobulin binding polypeptide comprises
 PT immunoglobulin-like domain containing scaffold and exhibits selective
 PT binding activity, for producing non-immunoglobulin binding polypeptides
 PT with selective binding activity.
 XX
 PS Disclosure; SEQ ID NO 6; 45pp; English.

XX The invention relates to a novel chimeric non-immunoglobulin binding
 CC polypeptide. The polypeptide comprises an immunoglobulin-like domain
 CC containing scaffold with two or more solvent exposed loops containing a
 CC different complementarity-determining region (CDR) from a parent antibody
 CC inserted into each of the loops and exhibiting selective binding activity
 CC toward a ligand bound by the parent antibody. The invention further
 CC comprises: a chimeric ThyOx binding polypeptide, comprising one or more
 CC altered immunoglobulin-like domain loop regions of a ThyOx family
 CC polypeptide or at least one immunoglobulin-like domain containing

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Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	424	70.1	161	2	T47130	hypothetical prote	
2	422	69.8	161	1	TDHU	Thy-1 membrane gly	
3	291.5	48.2	162	1	TDMS	Thy-1 membrane gly	
4	280	46.3	161	1	TDRT	Thy-1 membrane gly	
5	176.5	29.2	160	2	A48975	Thy-1 glycoprotein	
6	132	21.8	111	2	S25048	Ig heavy chain V r	
7	130	21.5	111	2	S25045	Ig heavy chain V r	
8	129	21.3	116	2	S53751	antibody Fab Jel 1	
9	126.5	20.9	120	2	S25175	Ig heavy chain V r	
10	126	20.8	120	2	S41394	Ig heavy chain V r	
11	124	20.5	69	2	S25150	Ig heavy chain V r	
12	123	20.3	106	2	S25036	Ig heavy chain V r	
13	122.5	20.2	123	2	S20646	Ig heavy chain V r	
14	122	20.2	98	2	PH1164	Ig heavy chain V r	
15	122	20.2	111	2	S25054	Ig heavy chain V r	
16	122	20.2	111	2	S25052	Ig heavy chain V r	
17	121	20.0	98	2	PH1160	Ig heavy chain V r	
18	120	19.8	111	2	S25032	Ig heavy chain V r	
19	120	19.8	111	2	S26463	Ig heavy chain V r	
20	120	19.8	139	2	PS0024	Ig heavy chain pre	
21	119	19.7	102	2	S25025	Ig heavy chain - m	
22	119	19.7	106	2	PH1005	Ig heavy chain V r	
23	119	19.7	111	2	S25024	Ig heavy chain V r	
24	118.5	19.6	109	2	S26318	Ig heavy chain V r	
25	118	19.5	109	2	S25038	Ig heavy chain V r	
26	118	19.5	111	2	S25055	Ig heavy chain V r	
27	117	19.3	111	2	S25033	Ig heavy chain V r	
28	117	19.3	111	2	S25034	Ig heavy chain V r	
29	116	19.2	87	2	PH1162	Ig heavy chain V r	

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein; thymocyte; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-161/Product: Thy-1 membrane glycoprotein #status predicted <MAT>
F:20-141/Domain: extracellular #status predicted <EX1>
F:31-106/Domain: immunoglobulin homology <IMM>
F:142-161/Domain: transmembrane #status predicted <TMW>
F:42-119,139/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 69.8%; Score 422; DB 1; Length 161;
Best Local Similarity 73.3%; Pred. No. 3.3e-34;
Matches 88; Conservative 3; Mismatches 11; Indels 18; Gaps 3;

QY 1 QVSRGQKVTSLTACLVDSQSLRDLCDCHRENTSSNYMHFSLTRETKKHVLFGTID-PADSY 59
Db 15 QVSRGQKVTSLTACLVDSQSLRDLCDCHRENTSSPIQYEFSLTRETKKHVLFGVGVPEHTY 74

QY 60 TSYNQF-----KDEGTYTCALHSHSGHSPPISSQNVTVLRLDKLVKCGV 103
Db 75 RS-RTNFTSKYHKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRLDKLVKCGI 133

RESULT 3
TDSM
Thy-1 membrane glycoprotein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jul-1982 #sequence revision 28-May-1986 #text change 09-Jul-2004
C:Accession: A94278; A24647; A94265; I59028; I55957; A03108
R:Seiki, T.; Chang, H.C.; Moriuchi, T.; Denome, R.; Ploegh, H.; Silver, J.
Science 227, 649-651, 1985
A:Title: A hydrophobic transmembrane segment at the carboxyl terminus of Thy-1.
A:Reference number: A94278; MUID:85115360; PMID:2857501
A:Accession: A94278
A:Molecule type: DNA
A:Residues: 1-162 <SIG>
A:Cross-references: UNIPARC:UPI000002395E
R:Guiguerre, V.; Isobe, K.I.; Grosveld, F.
EMBO J. 4, 2017-2024, 1985
A:Title: Structure of the murine Thy-1 gene.
A:Reference number: A24647; MUID:86055760; PMID:2866091
A:Contents: Thy-1.2 allotype
A:Accession: A24647
A:Molecule type: DNA
A:Residues: 1-162 <GIG>
A:Cross-references: UNIPARC:UPI000002395E
R:Williams, A.F.; Gagnon, J.
Science 216, 696-703, 1982
A:Title: Neuronal cell Thy-1 glycoprotein: homology with immunoglobulin.
A:Reference number: A94265; MUID:82199396; PMID:6177036
A:Accession: A94265
A:Molecule type: protein
A:Residues: 20-131 <WIL>
A:Cross-references: UNIPARC:UPI0000173745
A:Note: the Thy-1.1 sequence differs from that shown in having 108-Arg
R:Chang, H.
Proc. Natl. Acad. Sci. U.S.A. 82, 3819-3823, 1985
A:Title: Isolation and characterization of mouse Thy-1 genomic clones.
A:Reference number: I59028; MUID:85216583; PMID:2582427
A:Accession: I59028
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-162 <RES>
A:Cross-references: UNIPARC:UPI000002395E; GB:M1160; NID:G202034; PIDN:AAA40441.1; PID:
R:Ingraham, H.A.; Lawless, G.M.; Evans, G.A.
J. Immunol. 136, 1482-1489, 1986
A:Title: The mouse Thy-1.2 glycoprotein gene: Complete sequence and identification of ar
A:Reference number: I55957; MUID:86113437; PMID:2868059
A:Accession: I55957
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-162 <RE2>
A:Cross-references: UNIPARC:UPI000002395E; GB:M12379; NID:G202040; PIDN:AAA40443.1; PID:

C:Comment: The Thy-1.2 sequence is shown.
C:Genetics:
A:Map position: 9
A:Introns: 13/1; 126/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein; pyroglutamic acid; T-cell; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-162/Product: Thy-1 membrane glycoprotein #status predicted <MAT>
F:31-107/Domain: immunoglobulin homology <IMM>
F:143-162/Domain: transmembrane #status predicted <TMW>
F:20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimer
F:28-131,138-105/Disulfide bonds: #status experimental
F:42,94,118/Binding site: carbohydrate (Aan) (covalent) #status experimental

Query Match 48.2%; Score 291.5; DB 1; Length 162;
Best Local Similarity 55.8%; Pred. No. 2e-21;
Matches 67; Conservative 13; Mismatches 23; Indels 17; Gaps 5;

QY 1 QVSRGQKVTSLTACLVDSQSLRDLCDCHRENTSSNYMH-FSLTRETKKHVLFGTID-PADS 58
Db 15 QVSRGQKVTSLTACLVNQNLCDCHRENTXDNSIQHFEFSLTREKKHVLSTGIGIPEHT 74

QY 59 Y-----TSYNQ-----NF--KDEGTYTCALHSHSGHSPPISSQNVTVLRLDKLVKCGV 103
Db 75 YRSRVTLNQPVIKVLTLANFTTKDEGDYFCELVQSGANPWSNKSISVYRDKLVKCGI 134

RESULT 4
TDSM
Thy-1 membrane glycoprotein precursor - rat
N:Alternate names: thy-1 antigen
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-Jun-1981 #sequence revision 08-Feb-1996 #text change 09-Jul-2004
C:Accession: B45909; A45909; A25255; A21652; A90311; A93296; A02107
R:Seiki, T.; Moriuchi, T.; Chang, H.C.; Denome, R.; Silver, J.
Nature 313, 485-487, 1985
A:Title: Structural organization of the rat thy-1 gene.
A:Reference number: A45909; MUID:85111162; PMID:2857477
A:Accession: B45909
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-161 <SEK>
A:Cross-references: UNIPROT:P01830; UNIPARC:UPI0000136P21; GB:X02002; NID:G57363; PIDN:
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 20-161 <SE2>
R:Seiki, T.; Chang, H.C.; Moriuchi, T.; Denome, R.; Silver, J.
Fed. Proc. 44, 2865-2869, 1985
A:Title: Thy-1: a hydrophobic transmembrane segment at the carboxyl terminus.
A:Reference number: A25255; MUID:86005549; PMID:2864289
A:Accession: A25255
A:Molecule type: DNA
A:Residues: 1-70,'Q',72-161 <SE3>
A:Cross-references: UNIPARC:UPI00000170B3E; GB:X03152; NID:G57357; PIDN:CAA26931.1; PID:
R:Moriuchi, T.; Silver, J.
FEBS Lett. 178, 105-107, 1984
A:Title: Rat Thy-1 antigen has a hydrophobic segment at the carboxyl terminus.
A:Reference number: A21652; MUID:85051865; PMID:6149956
A:Accession: A21652
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 20-161 <MOR>
A:Cross-references: UNIPARC:UPI0000170B3F; GB:X03150; GB:J00792; GB:X01445
R:Campbell, D.G.; Gagnon, J.; Reid, K.B.M.; Williams, A.F.
Biochem. J. 195, 15-30, 1981
A:Title: Rat brain Thy-1 glycoprotein. The amino acid sequence, disulphide bonds and an
A:Reference number: A90311; MUID:82068190; PMID:6118137
A:Accession: A90311
A:Molecule type: protein
A:Residues: 20-130 <CAM>
A:Cross-references: UNIPARC:UPI00000173743

A>Note: this sequence shows homologies with immunoglobulin domains
 R:Moriuchi, T.; Chang, H.C.; Denome, R.; Silver, J.
 Nature 301, 80-82, 1983
 A>Title: Thy-1 cDNA sequence suggests a novel regulatory mechanism.
 A:Reference number: A93296; MUID:83115223; PMID:6130472
 A:Accession: A93296
 A:Molecule type: mRNA
 A:Residues: 1-122 <MO2>
 A:Cross-references: UNIPARC:UPI0000173744
 A:Comment: This glycoprotein is a major constituent of brain-cell membrane and is abundant in the brain.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein; membrane protein; pyroglyutamic acid
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-130/Product: thy-1 membrane glycoprotein #status experimental <MAT>
 F:31-106/Domain: immunoglobulin homology <IMM>
 F:50/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status experimental
 F:28-130,38-104/Disulfide bonds: #status experimental
 F:42,93,117/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 46.3%; Score 280; DB 1; Length 161;
 Best Local Similarity 50.4%; Pred. No. 2.7e-20;
 Matches 60; Conservative 16; Mismatches 27; Indels 16; Gaps 3;
 QY 1 QVSRGKVTSLTACLVDSQLRLDCHRENTSSSNVMMHFSLTRTKKHLVFGTID-PADSY 59
 DB 15 QMSRGQVSLTACLVDSQLRLDCHRENTSSSNVMMHFSLTRTKKHLVFGTID-PADSY 74
 QY 60 TS-----YQNF-----KDEGTYTCALHSGHSPPISSQNVTVLRDLKLVCEGV 103
 DB 75 RSRVNLFSDFIKVTLNFTTKDEGYMCELRSVQNPSSNKTINVRDLKLVKCGGI 133

RESULT 5
 A48975
 Thy-1 glycoprotein - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: A48975
 R:Dowsing, B.J.; Gooley, A.A.; Gunning, P.; Cunningham, A.; Jeffrey, P.L.
 Brain Res. Mol. Brain Res. 14, 250-260, 1992
 A>Title: Molecular cloning and primary structure of the avian Thy-1 glycoprotein.
 A:Reference number: A48975; MUID:93061794; PMID:1359371
 A:Accession: A48975
 A>Status: preliminary
 A:Molecule type: mRNA; protein
 A:Residues: 1-160 <DOM>
 A:Cross-references: UNIPROT:Q07212; UNIPARC:UPI0000136F1D; GB:LL4924; NID:G289826; PIDN:
 A>Note: sequence extracted from NCBI backbone (NCBI:117489, NCBI:117490)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein

Query Match 29.2%; Score 176.5; DB 2; Length 160;
 Best Local Similarity 36.2%; Pred. No. 3.7e-10;
 Matches 42; Conservative 22; Mismatches 35; Indels 17; Gaps 4;
 QY 1 QVSRGKVTSLTACLVDSQLRLDCHRENTSSSNVMMHFSLTRTKKHLVFGTID-PADSY 59
 DB 15 QAARCMIRLSACLVDSQLRLDCHRENTSSSNVMMHFSLTRTKKHLVFGTID-PADSY 73
 QY 60 TS-----YQNF-----KDEGTYTCALHSGHSPPISSQNVTVLRDLKLVK 100
 DB 74 RNRANVTMKNLVLYLHSTTSDEGYMCELKATNDYTNQIKNITVIRDLKLVK 129

RESULT 6
 S25048
 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 20-Jun-2000
 C:Accession: S25048; S25046; S25049
 R:Jacob, J.; Kelsoe, G.
 submitted to the EMBL Data Library, July 1992
 A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl)

A:Reference number: S25024
 A:Accession: S25048
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-111 <JAC1>
 A:Cross-references: UNIPARC:UPI000011609E; EMBL:X67349; NID:G50898; PIDN:CAA47764.1; PI:
 A:Accession: S25046
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-111 <JAC2>
 A:Cross-references: UNIPARC:UPI000011609E; EMBL:X67346; NID:G50894; PIDN:CAA47761.1; PI:
 A:Accession: S25049
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-97, 'GSSL', 102-111 <JAC3>
 A:Cross-references: UNIPARC:UPI00001160A0; EMBL:X67350; NID:G50900; PIDN:CAA47765.1; PI:
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 21.8%; Score 132; DB 2; Length 111;
 Best Local Similarity 33.3%; Pred. No. 5.6e-06;
 Matches 31; Conservative 13; Mismatches 47; Indels 2; Gaps 1;
 QY 19 SLRLDCRHEHTSSSNVMMHFSLTRTKKHLVFGTID-PADSYTSYNQNFKDEGTYTCALHH 78
 DB 13 SVLSCKASGYTFTSWMHVVKQRPGRGLEWIGRIDPNSGGTKYNEKFSKATLTVDKPS 72
 QY 79 SGHSPPPISSQNVTVLRDLKLVCEGVYRYFYDY 111
 DB 73 STAYMQLSS--LTSEDSAVVYCARYYVYFYDY 103

RESULT 7
 S25045
 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 20-Jun-2000
 R:Jacob, J.; Kelsoe, G.
 submitted to the EMBL Data Library, July 1992
 A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl)
 A:Reference number: S25024
 A:Accession: S25045
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-111 <JAC>
 A:Cross-references: UNIPARC:UPI000011609D; EMBL:X67345; NID:G50892; PIDN:CAA47760.1; PI:
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 21.5%; Score 130; DB 2; Length 111;
 Best Local Similarity 33.3%; Pred. No. 8.8e-06;
 Matches 31; Conservative 13; Mismatches 47; Indels 2; Gaps 1;
 QY 19 SLRLDCRHEHTSSSNVMMHFSLTRTKKHLVFGTID-PADSYTSYNQNFKDEGTYTCALHH 78
 DB 13 SVLSCKASGYTFTSWMHVVKQRPGRGLEWIGRIDPNSGGTKYNEKFSKATLTVDKPS 72
 QY 79 SGHSPPPISSQNVTVLRDLKLVCEGVYRYFYDY 111
 DB 73 STAYMQLSS--LTSEDSAVVYCARYYVYFYDY 103

RESULT 8
 S53751
 antibody Fab Jcl 103 heavy chain - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 31-Dec-2004
 C:Accession: S53751
 R:Pokkuluri, P.R.; Bouthillier, F.; Li, Y.; Kuderova, A.; Lee, J.; Cygler, M.
 J. Mol. Biol. 243, 283-297, 1994

S20646

IG heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C:Accession: S20646
 R:Lozman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
 submitted to the EMBL Data Library, February 1992
 A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
 A:Reference number: S20639
 A:Accession: S20646
 A>Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-123 <LOS>
 A:Cross-references: UNIPARC:UPI0000116020; EMBL:X65001; NID:g52612; PIDN:CAA46134.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 20.2%; Score 122.5; DB 2; Length 123;
 Best Local Similarity 30.9%; Pred. No. 5.3e-05;
 Matches 30; Conservative 16; Mismatches 36; Indels 15; Gaps 3;

QY 19 SLRLDCRHEHTSSSNYMHFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGTYTTCALHH 78

DB 17 SVKLSCKASGYTFTSYWVHWVKQRPQGLEWIGETAPSDNYTYNQNFKDEGTYTTCALHH 73

QY 79 SGHSPPISSQNVTLRLDKLVKCR--GVYY--RYVFD 110

DB 74 -----KSNAYMQLSLSLTSSEDSAIYICSRRYVD 103

RESULT 14

PH1164
 IG heavy chain V region (clone 37F.2A) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH1164
 R:Schitteck, B.; Rajewsky, K.
 J. Exp. Med. 176, 427-438, 1992
 A>Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
 A:Reference number: PH1105; MUID:92364545; PMID:1500855
 A:Accession: PH1164
 A:Molecule type: DNA
 A:Residues: 1-98 <SCH>
 A:Cross-references: UNIPARC:UPI0000176BC6
 A:Experimental source: B cell
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 20.2%; Score 122; DB 2; Length 98;
 Best Local Similarity 41.8%; Pred. No. 4.6e-05;
 Matches 23; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 19 SLRLDCRHEHTSSSNYMHFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGTYT 73

DB 17 SVKLSCKASGYTFTSYWVHWVKQRPQGLEWIGNIDPSDSETHYNQKFKDKATLT 71

RESULT 15

S25054
 IG heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 20-Jun-2000
 C:Accession: S25054
 R:Jacob, J.; Kelsoe, G.
 submitted to the EMBL Data Library, July 1992
 A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitropheny
 A:Reference number: S25024
 A:Accession: S25054
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-111 <JAC>

A:Cross-references: UNIPARC:UPI00001160A4; EMBL:X67358; NID:g50921; PIDN:CAA47771.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 20.2%; Score 122; DB 2; Length 111;
 Best Local Similarity 32.3%; Pred. No. 5.3e-05;
 Matches 30; Conservative 13; Mismatches 48; Indels 2; Gaps 1;

QY 19 SLRLDCRHEHTSSSNYMHFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGTYTTCALHH 78

DB 13 SVKLSCKASGYTFTSYWVHWVKQRPQGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPS 72

QY 79 SGHSPPISSQNVTLRLDKLVKCEGVYRYVFDY 111

DB 73 STAYMQLSS--LTSSEDSAVTYCARYYGYGYFDY 103

Search completed: December 6, 2005, 10:42:44
 Job time : 19.5645 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 6, 2005, 10:32:17 ; Search time 87.0209 Seconds
(without alignments)
532.965 Million cell updates/sec

Title: US-10-611-655-4
Perfect score: 605
Sequence: 1 QVSRGQKVTSLTACLVDSQL.....VLRDKLVKCEGVYRYFYDY 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	605	100.0	111	5	US-10-611-655-4
2	425	70.2	159	4	US-10-322-281-20
3	424	70.1	161	4	US-10-165-603-32
4	424	70.1	161	4	US-10-794-899-66
5	424	70.1	161	5	US-10-287-436A-449
6	424	70.1	161	5	US-10-287-436A-1149
7	424	70.1	165	3	US-09-925-301-1384
8	424	70.1	165	4	US-10-106-698-4624
9	422	69.8	161	3	US-09-918-715-220
10	422	69.8	161	4	US-10-474-794-220
11	422	69.8	161	5	US-10-979-159-220
12	402.5	66.5	162	5	US-10-611-655-1
13	398	65.8	176	5	US-10-611-655-10
14	398	65.8	334	5	US-10-611-655-6
15	398	65.8	334	5	US-10-611-655-8
16	293.5	48.5	158	4	US-10-322-281-17
17	291.5	48.2	162	3	US-09-918-715-303
18	291.5	48.2	162	4	US-10-474-794-303
19	291.5	48.2	162	5	US-10-979-159-303
20	291	48.1	171	5	US-10-450-763-49897
21	280	46.3	161	4	US-10-165-603-30
22	280	46.3	161	4	US-10-794-899-64
23	264.5	43.7	114	4	US-10-410-842A-4
24	186.5	30.8	124	5	US-10-611-655-2
25	162	26.8	51	5	US-10-450-763-49895
26	129.5	21.4	118	5	US-10-816-938-23
27	127.5	21.1	117	5	US-10-683-547-14

28	126	20.8	120	4	US-10-096-246-12	Sequence 12, Appl
29	124.5	20.6	116	3	US-03-940-727B-17	Sequence 17, Appl
30	123	20.3	113	3	US-09-940-727B-118	Sequence 118, Appl
31	123	20.3	121	5	US-10-879-994-82	Sequence 82, Appl
32	123	20.3	242	4	US-10-259-087A-18	Sequence 18, Appl
33	123	20.3	242	4	US-10-689-006-18	Sequence 18, Appl
34	123	20.3	248	5	US-10-879-994-14	Sequence 14, Appl
35	123	20.3	248	5	US-10-610-452-14	Sequence 14, Appl
36	119.5	19.8	464	4	US-10-216-484-9	Sequence 9, Appl
37	119.5	19.8	464	4	US-10-384-933-9	Sequence 9, Appl
38	118	19.5	104	6	US-10-032-482-1	Sequence 1, Appl
39	118	19.5	104	6	US-11-129-359-1	Sequence 1, Appl
40	118	19.5	121	4	US-10-643-857-2	Sequence 2, Appl
41	118	19.5	121	5	US-10-524-134-2	Sequence 2, Appl
42	116	19.2	114	4	US-10-803-622-226	Sequence 226, Appl
43	116	19.2	114	4	US-10-803-653-226	Sequence 226, Appl
44	116	19.2	118	5	US-10-937-046-9	Sequence 9, Appl
45	115.5	19.1	145	4	US-10-216-484-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1
US-10-611-655-4
; Sequence 4, Application US/10611655
; Publication No. US20040266993A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides
; FILE REFERENCE: 66663-026
; CURRENT APPLICATION NUMBER: US/10/611,655
; CURRENT FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ThyOx non-immunoglobulin binding polypeptide
US-10-611-655-4

Query Match	100.0%	Score 605;	DB 5;	Length 111;
Best Local Similarity	100.0%	Pred. No. 1e-56;		
Matches 111;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	QVSRGQKVTSLTACLVDSQLRDLCHENTSSSNYMHFSLTRETXXHVLFGTIDPADSYT	60	
Db	1	QVSRGQKVTSLTACLVDSQLRDLCHENTSSSNYMHFSLTRETXXHVLFGTIDPADSYT	60	
QY	61	SYNPFKDEGTTCALHSHGSPPISSQNVTVLRDKLVKCEGVYRYFYDY	111	
Db	61	SYNPFKDEGTTCALHSHGSPPISSQNVTVLRDKLVKCEGVYRYFYDY	111	
RESULT 2				
US-10-322-281-20				
; Sequence 20, Application US/10322281				
; Publication No. US20040126762A1				
; GENERAL INFORMATION:				
; APPLICANT: David W. Morris				
; APPLICANT: Marc S. Malandaro				
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer				
; FILE REFERENCE: 529452001000				
; CURRENT APPLICATION NUMBER: US/10/322,281				
; CURRENT FILING DATE: 2002-12-17				
; NUMBER OF SEQ ID NOS: 866				
; SOFTWARE: FastSeq for Windows Version 4.0				
; SEQ ID NO 20				
; LENGTH: 159				
; TYPE: PRT				
; ORGANISM: Homo sapiens				

Db 15 QVSRGQKVTSLTACLVDSRLDCRHSNTSSPIQVEFSLTRETCKHVLFGTVGVPEHTY 74
 QY 60 TSYNQNF-----KDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCGV 103
 Db 75 RS-RTNFTSKYHKMVKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCGI 133

RESULT 11
 US-10-979-159-220
 ; Sequence 220, Application US/10979159
 ; Publication No. US20050142138A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brad St. Croix
 ; APPLICANT: Bert Vogelstein
 ; APPLICANT: Kenneth Kinzler
 ; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
 ; FILE REFERENCE: 1107.00134
 ; CURRENT FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: US/09/918,715
 ; PRIOR FILING DATE: 2001-08-01
 ; PRIOR APPLICATION NUMBER: 60/222,599
 ; PRIOR FILING DATE: 2000-08-02
 ; PRIOR APPLICATION NUMBER: 60/224,360
 ; PRIOR FILING DATE: 2000-08-11
 ; PRIOR APPLICATION NUMBER: 60/282,850
 ; PRIOR FILING DATE: 2000-04-11
 ; NUMBER OF SEQ ID NOS: 358
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 220
 ; LENGTH: 161
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-979-159-220

Query Match 69.8%; Score 422; DB 5; Length 161;
 Best Local Similarity 73.3%; Pred. No. 6e-37;
 Matches 88; Conservative 3; Mismatches 11; Indels 18; Gaps 3;
 QY 1 QVSRGQKVTSLTACLVDSRLDCRHSNTSSPIQVEFSLTRETCKHVLFGTVGVPEHTY 59
 Db 15 QVSRGQKVTSLTACLVDSRLDCRHSNTSSPIQVEFSLTRETCKHVLFGTVGVPEHTY 74
 QY 60 TSYNQNF-----KDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCGV 103
 Db 75 RS-RTNFTSKYHKMVKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCGI 133

RESULT 12
 US-10-611-655-1
 ; Sequence 1, Application US/10611655
 ; Publication No. US20040266993A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Evans, Glen A.
 ; TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides
 ; FILE REFERENCE: 66663-026
 ; CURRENT FILING DATE: 2003-06-30
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 162
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-611-655-1

Query Match 66.5%; Score 402.5; DB 5; Length 162;
 Best Local Similarity 71.9%; Pred. No. 7.4e-35;
 Matches 87; Conservative 3; Mismatches 12; Indels 19; Gaps 4;
 QY 1 QVSRGQKVTSLTACLVDSRLDCRHSNTSSPIQVEFSLTRETCKHVLFGTVGVPEHTY 59

Db 15 QVSRGQKVTSLTACLVDSRLDCRHSNTSSPIQVEFSLTRETCKHVLFGTVGVPEHTY 74
 QY 60 TSYNQNF-----KDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCGI 102
 Db 75 RS-RTNFTSKYHKMVKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCGI 133
 QY 103 V 103
 Db 134 I 134

RESULT 13
 US-10-611-655-10
 ; Sequence 10, Application US/10611655
 ; Publication No. US20040266993A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Evans, Glen A.
 ; TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides
 ; FILE REFERENCE: 66663-026
 ; CURRENT FILING DATE: 2003-06-30
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10
 ; LENGTH: 176
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: chimeric ThyOx carrier polypeptide containing
 ; OTHER INFORMATION: glucagon-like peptide 1
 US-10-611-655-10

Query Match 65.8%; Score 398; DB 5; Length 176;
 Best Local Similarity 72.2%; Pred. No. 2.5e-34;
 Matches 83; Conservative 3; Mismatches 11; Indels 18; Gaps 3;
 QY 6 QKVTSLTACLVDSRLDCRHSNTSSPIQVEFSLTRETCKHVLFGTVGVPEHTY 64
 Db 49 QKVTSLTACLVDSRLDCRHSNTSSPIQVEFSLTRETCKHVLFGTVGVPEHTY 107
 QY 65 NF-----KDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCGI 103
 Db 108 NFKTYHKMVKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCGI 162

RESULT 14
 US-10-611-655-6
 ; Sequence 6, Application US/10611655
 ; Publication No. US20040266993A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Evans, Glen A.
 ; TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides
 ; FILE REFERENCE: 66663-026
 ; CURRENT FILING DATE: 2003-06-30
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 334
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: chimeric ThyOx carrier polypeptide containing
 ; OTHER INFORMATION: erythropoietin
 US-10-611-655-6

Query Match 65.8%; Score 398; DB 5; Length 334;
 Best Local Similarity 72.2%; Pred. No. 5.3e-34;
 Matches 83; Conservative 3; Mismatches 11; Indels 18; Gaps 3;
 QY 6 QKVTSLTACLVDSRLDCRHSNTSSPIQVEFSLTRETCKHVLFGTVGVPEHTY 64
 Db 207 QKVTSLTACLVDSRLDCRHSNTSSPIQVEFSLTRETCKHVLFGTVGVPEHTY 265

Qy 65 NP-----KDEGTYTCALHSHGSPPISSQNVTVLRLDKLVKCEGV 103
||
Db 266 NFKSKYHMKVLYLSAFTSKDEGTYTCALHSHGSPPISSQNVTVLRLDKLVKCEGI 320

RESULT 15

US-10-611-655-8
; Sequence 8, Application US/10611655
; Publication No. US2004026693A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides
; FILE REFERENCE: 66663-026
; CURRENT APPLICATION NUMBER: US/10/611,655
; CURRENT FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SuperEpo
US-10-611-655-8

Query Match 65.8%; Score 398; DB 5; Length 334;
Best Local Similarity 72.2%; Pred. No. 5.3e-34;
Matches 83; Conservative 3; Mismatches 11; Indels 18; Gaps 3;

Qy 6 QKVTSLTACLVDQSLDCRHEHTSSNTYMHFSLRTETKKHVLFGTID-PADSYTSYNO 64
||
Db 207 QKVTSLTACLVDQSLDCRHEHTSSNTYMHFSLRTETKKHVLFGTGVPEHTYRS-RT 265

Qy 65 NP-----KDEGTYTCALHSHGSPPISSQNVTVLRLDKLVKCEGV 103
||
Db 266 NFKSKYHMKVLYLSAFTSKDEGTYTCALHSHGSPPISSQNVTVLRLDKLVKCEGI 320

Search completed: December 6, 2005, 10:47:47
Job time : 88.0209 secs

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